

Human DNase I

```
PRI
                                                               06-MAR-1995
                         1039 bp
                                    mRNA
LOCUS
            HUMDNASEI
            Human DNase I mRNA, complete cds.
DEFINITION
ACCESSION
            M55983
            M55983.1 GI:181623
VERSION
            DNase I.
KEYWORDS
SOURCE
            Human pancreus, cDNA to mRNA.
  ORGANISM
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
               (bases 1 to 1039)
REFERENCE
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
            91067672
  MEDLINE
                     Location/Qualifiers
FEATURES
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                      DAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLI
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                      VEVMLK"
                      160..1008
     gene
                      /gene="DNase I"
                      226..1005
     mat peptide
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                                            226 t
BASE COUNT
                 226 a
                          305 c
                                   282 q
ORIGIN
        1 tectgeacag geagtgeett gaagtgette tteagagace tttetteata gaetaetttt
       61 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
      121 cattetegte atetetgagg acateaceat cateteagga tgaggggeat gaagetgetg
      181 ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgcagcc
      241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
      301 gtgcagatec tgageegeta tgaeategee etggteeagg aggteagaga eageeaeetg
      361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
      421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
       481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
       541 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc
       601 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
       661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg
       721 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc
       781 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca
       841 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgccgtt
       901 gttoccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg
       961 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc
      1021 cacaccagtt gaactgcag
```

FIGURE 2

11

hyeran DNAse I comornios

```
LOCUS
             MHDNASE.DN
                             783 bp
                                        mPNA
                                                          PRI
                                                                      06-MAR-1995
             Human DNase I mRNA, complete cds, Mature sequence modified to remove Narl site
DEFINITION
             M55963
ACCESSION
NID
              g181623
KEYWORDS
             DNase I.
SOURCE
             Human pancreus, cUNA to mRNA.
  ORGANISM
             Homo sapiens
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
             1 (bases 1 to 1039)
             Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. Recombinant human DNase I reduces the viscosity of cystic fibrosis
  AUTHORS
  TITLE
  JOURNAL
             Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  MEDLINE
              91067672
FEATURES
                       Location/Qualifiers
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                        /clone="hDNase-18-1"
                        /tissue_type="pancreas"
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      sig_peptide
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                        160. .1008
      CDS
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                        PCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGL
                        EDVMLMGDFNAGCSYVRPSQNSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG
                        MLLRGAVVPDSALEFNEQAAYGLSDQLAQA1SDHYPVEVMT.K*
                        160. .1008
      aeue
                        /gene="DNase I'
      mat_peptide
                        226. .1005
                        /gene="DNase I"
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BASE COUNT
                  168 a
                            236 c
                                      220 g
                                                 159 t
ORIGIN
         1 CIGARGATCG CAGCCTICAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
        61 CICGICAGCI ACATIGIGCA GATCCIGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGIC
       121 AGAGACAGCC ACCIGACIGC CGIGGGGAAG CIGCIGGACA ACCICAAICA GGACGCACCA
       181 GACACCTATC ACTACGTGGT CACTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
       241 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
301 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
       361 COGTTCACAG AGGTCAGGGA GITIGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA 421 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
       481 GAGGACGICA IGITGAIGGG CGACTICAAI GCGGGCTGCA GCIAIGTGAG ACCCTCCCAG
       541 TGGTCATCCA ICCGCCTGTG GACAAGCCCC ACCTICCAGT GGCTGATCCC CGACAGCGCT
       601 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
       661 CICCGAGGGG CCGITGITCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
       721 CIGAGIGACC AACIGGCCCA AGCCATCAGI GACCACTAIC CAGIGGAGGI GAIGCIGAAG
       781 TGA
```



841 GAGGTGATGC TGAAGTGA

FIGURE 2(B)



```
29-AUG-2000
                                                     SYN
                          858 BP SS-DNA
            PAS155 GB.
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
                     Location/Qualifiers
FEATURES
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     frag
                     /note="1 to 1039 of M55983.DNA [Split]"
                     <10..>75
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                      /db_xref="taxon:9606"
                      /clone="hDNase-18-1"
                      /tissue type="pancreas [Split]"
                      10..75
     sig peptide
                      /qene="DNase I"
                      10..>75
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                      /codon start="1"
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                      LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
                      D... [Split]"
                      10..>75
     gene
                      /gene="DNase I [Split]"
                      76..858
      frag
                      /note="1 to 783 of mod humanDNAseI"
                      76..858
      frag
                      /note="1 to 72 of 104linker"
                      join(76..>129,<131..147)
      frag
                      /note="1 to 72 of 103linker [Split]"
                      join(76..>126,<127..>129,<131..147)
      frag
                      /note="1 to 78 of 102linker [Split]"
                                                        0 OTHER
                          260 C
                                    251 G
                                             170 T
 BASE COUNT
                 177 A
 ORIGIN
         1 GCCGCCACCA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC GGCCCTACTG
        61 CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG
       121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC
       181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC
       241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC
       301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC
       361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT
       421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG
       481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA
       541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT
       601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG
       661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG
       721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC
       781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG
```

//

(A) pAS6 - light drain

```
LOCUS
              HMFGllC2.D
                                721 bp
                                            DNA
DEFINITION HUMANISED HMFG1 LIGHT CHAIN VOD LEADER.
ACCESSION .
Keywords
SOURCE
  ORGANISM
REFERENCE
                  (BASES 1 TO 342)
  AUTHORS
              VERHOEYEN ET AL
              CONSTRUCTION OF RESHAPED HMFG1 ETC IMMUNOL. (1993):78, 364-370 SCANNED IN FROM JOURNAL
  TITLE
  JOURNAL
COMMENT
FEATURES
  SITES
```

This is the sequence of the HMFG1 light chain gene with the Vnp leader sequence attached. Translate from residue 1. Note residue 399 is T > A in all clones leading to R133 silent mutation (T in Verhoeyen paper)

EASE COUNT 197 a 202 c 162 g 140 t
ORIGIN 7
LEADER SEQ

<u> </u>		MIDGE				
`1	ATGGGATGGA	GCTGTATCAT	CCTCTTCTTG	GTAGCAACAG	CTACAGGTGT	CCACTCCGAC
61	ATCCAGATGA	CCCAGAGCCC	AAGCAGCCIG	AGCGCCAGCG	TGGGTGACAG	AGTGACCATC
121	ACCTGTAAGT	CCAGTCAGAG	CCTTTTATAT	AGTAGCAATC	AAAAGATCTA	CTTGGCCTGG
181	TACCAGCAGA	AGCCAGGTAA	GGCTCCAAAG	CTGCTGATCT	ACTGGGCATC	CACTAGGGAA
241	TCTGGTGTGC	CANGCAGATT	CAGCGGTAGC	GGTAGCGGTA	CCGACTTCAC	CTTCACCATC
301	AGCAGCCTCC	AGCCAGAGGA	CATCGCCACC	TACTACTGCC	AGCANTATTA	TAGATATCCT
361	CCGACGTTCG	GCCAAGGGAC	CAAGGTGGAA	ATCAAACGAA	CTGTGGCTGC	ACCATCTGTC
421	TICATCTICC	CGCCATCTGA	IGAGCAGTIG	AAATCTGGAA	CIGCCICIGI	TGTGTGCCTG
481	CIGNATANCI	TCTATCCCAG	AGAGGCCAAA	GTACAGTGGA	AGGTGGATAA	CCCCCTCCAA
541	ICGGGTAACT	CCCAGGAGAG	TGTCACAGAG	CAGGACAGCA	AGGACAGCAC	CTACAGCCTC
601	AGCAGCACCC	TGACGCTGAG	CAAAGCAGAC	TACGAGAAAC	ACANAGTOTA	CCCCTCCCAÀ
661	GTCACCCATC	AGGGCCTGAG	CTCGCCCGTC	ACAAAGAGCT	TCAACAGGGG	AGAGTGTTAG
721	አ					

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Figure 3(B)



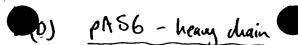
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29-AUG-2000
            HHMFG1KLC
                          730 BP SS-DNA
                                                     SYN
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
FEATURES
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                         208 C
                                  184 G
                                            140 T
                198 A
** SE COUNT
ORIGIN
        1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
       61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
      121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC
      181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
      241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC
      301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
      361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
      421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
      481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
      541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
      601 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
      661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
      721 GAGTGTTAGA
11
```

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Figure 3 (c)

HMFG-1 light chain with Vnp Leader (shaded)

MGWSCHEFLVATATGVHSDIQMTQSPSSLSASVGDRVTITCKSSQSL LYSSNQKIYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT DFTFTISSLQPEDIATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC



```
LOCUS
                        HHMFG1HC.D
                                                1404 bp
DEFINITION HUMANISED HMFG1 heavy chain
ACCESSION HHMEGIH
KEYWORDS
SOURCE
    ORGANISM
REFERENCE
   AUTHORS
                        VERHOEYEN BY AL
                        CONSTRUCTION OF RESHAPED HMFG1 etc
    TITLE
    JOURNAL
                        IMMUNOL. (1993):78, 364-370
COMMENT
                        VH domain SCANNED IN FROM JOURNAL
                        AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES
                        Residue 963 is G > T leading to silent mutation in all clones
FEATURES
    SITES
BASE COUNT
                               333 a
                                                 439 c
                                                                  379 g
                                                                                    253 t
ORIGIN
                                                              LEAPER -
              1 ATGGGATEGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
           61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CITCAGTGCC TACTGGATAG AGTGGGTGGG CCAGGCTCCA
181 GGAAAGGCC TGCAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGCTCACA GGCCCAGGGT GACAGCACAT CCACAAACAC AGCCTACATG
301 GAGCTCACA GCCTGAGGTC TGAGGCACAA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
421 AAGGGCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAACA GCACCTCTC AGCCTCCACC
421 AAGGGCCAT CGCTCTTCCC CCTGGCACCC TCCTCCAACA GCACCTCTG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
541 GGCGCCCTGA CCAGCCCCT CCACACCTTC CCGGACCGG TACAGTCTC AGGACTCTAC
661 AACGTGAATC ACAACCCAG CAACACCTTC CCGGACCAGA AAGTTGAGCC CTACATCTGC
661 AACGTGAATC ACAACCCAG CAACACCACA GTGGACAAGA AAGTTGAGCC CAAAACTTGT
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGA CCACCGAACC CTGAGGTCACA
641 TGCGTGGTGG TGGACGTGA CCACCGAACC CTGAGGTCACA
641 TGCGTGGTGG TGGACGTGA CCACCGAACAC CTCATGTGC
651 AACGTGACTAC CCCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
641 TGCGTGGTGG TGGACGTGA CCACCGAACAC CTCATGACT CCCGGACCCC TGAGGTCACA
641 TGCGTGGTGG TGGACGTGA CCACCGAACAC CCTCATGACT CCCGGACCCC TGAGGTCACA
641 TGCGTGGTGG TGGACGTGA CCACCGAACAC CCTCATGACT CCCGGACCCC TGAGGTCACA
641 TGCGTGGTGG TGGACGTGA CCACCGAACAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
            841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
            901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
          961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
          1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
          1321 AACGTCTTCT CAIGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
          1381 CTCTCCCTGT CTCCGGGTAA ATGA
                                                                  A ANTIGODY DNINE FUSIONS Made HERE (34->39.)
                    End of lower hingerigion of HEAVY CHAIN.
                        Adoseq. Fab', Fusions were Made at this point.
                        Those with HYBRID HINGES ARE MITTINGD
                                                                                                                                      PORTHER
                                                              lie.
              THIS PART GACAAAACTGACACA

IS -> D K T H T
```

AFTER THIS SEQUENCE YOUGET THE
MYBRID HINGE & LINKER SEQUENCES
Thon DNAZEI (eg Fab-DNase construct pAS302)

Constructs pAS23/27

Constr	Constructs pAS34/37	AS34,	/37															
AS79 AS80	CCG GGT AAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC GAG AGG GAC AGA GGC CCA TIT CCC TCG CCG CCC GAC TIC TAG L S L S R G K G S G G L K I A A F N	3G G	A D	5 6 8 8 8	၁ ၁ ၁ ၁	SGT GA	AAA TTT K	စစ္တ ၁၁၁ ၁၂	A60 TC6	<u> </u>	888	Ord To Ord	A TTO	ATC TAG	GCA	ည္ပ 🚜	TIC	AAC N
	,		Ē	HMFC-	1			1	Ž	HNKER]	_			<u>-</u> 롲	hu DNAML [7 7%	
9tri	Constructs pAS35/38	4835/	38															
AS81	CCG ARA GGC AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC AGG GAC AGA GGC TTC AAC	ე ლ	ă Ç	ب و و	20 20 20 20 20 20 20 20 20 20 20 20 20 2	AA T	999	AGC	990	990	ST3	AAG	AIC	රි	၁၁૭	TTC	X	
, \l	7	3 7		2	A.	×) 	25	30	्र	-	×	₹	æ	V	[E4	2	ĺ
Stri	imped Constructs pas36/39	79ES4	/39			ر م ک	DG (deleter)] <u>F</u>	LINKER ()			-5	Z 2	hu ANARK I				1
AS83 AS84	GẠG AGG GẠC AGG GGC GGG CTG AAG ATC GCA GCC TTC AAC	. S.) ¥ '	୦ ଓ ଝୁନ	2000	800	AGC TCG	ပ္ပတ္သ	999	orc Gac	AAG	ATC	GCA	ပ္ပ်ပ္	TTC	AAC		
4	ZW.C.				<u>=</u> _/ -		,] = -	LINKEY	2	1	4	1	1 2	The Driver 1	. _	2	ኍ	
Q ((replay by) was	•				<u>کے</u>	as (Separ	唇										

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(() Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

		TGT CCA GCA CCA GAG GGG AGC GGG CTG AAG ATC GCA GCC TTC ACA GGT CGT GTC CCC TCG C P A P E G S G G L K I A A F	hu ONASE I	CCA GCA CCA GAG GGG GTG AAG ATC GCA GCC TTC GGT CGT CTC CCG P A P E G G L K I A A F	SHORT hu DINKOK I
Constructs pasio1/105 AS86 GCA CCT GAA/GGC GGG CTG AAG ATC GCA GCC TTC AAC AS87 GGT GGC ACG GGT COT GGA CTT CCG CCC GAC TTC TAG P P E	Constructs pas102/106 WARET hu CAPAGE [MUKER	AS88 AS89 CTG TIT IGA GTG TGT ACG ACA CAG CTC ACA GGT GGT GGT CTC GGT CTC CCC ACA GGT GGT CGT GGT CTC CCC AS89 CTG TIT IGA GTG TGT ACG ACA CAG CTC ACA GGT GGT CGT GGT CTC CCC AS89 CTG TIT IGA GTG TGT ACG ACA CAG CTC ACA GGT GGT CGT GTC CTC CCC ACA GGT CGT CGT CTC CCC ACA GGT CGT CTC CCC ACA GGT CGT CTC ACA GGT CGT CGT CGT CTC CCC ACA GGT CGT CGT CTC CCC ACA GGT CGT CGT CTC CCC ACA GGT CGT CGT CGT CTC CCC ACA GGT CGT CGT CTC CCC ACA GGT CGT CTC CCC ACA GGT CGT CGT CTC CCC ACA GGT CTC ACA GGT CT	Constructs pas103/107	GTG TGT ACG ACA TGT CCA CCG TGT GTG TGT ACG ACA CAG CTC ACA GGT GGC ACA H I C C V E C P P C	HYBRID HINGE SP

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(A) pAS23

06-MAR-1995 1554 bp mRNA PRT PAS23. DNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I (construct 1) DEFINITION ACCESSION NID KEYWORDS DNase I. DNase I sequence is from assembled oligos (thus modified c/fSOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE 344 a 434 g 308 t 468 c BASE COUNT

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ORIGIN





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     § 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
     601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
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Figure S (c)

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                                           309 T
                345 A
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11.
      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
EF
      421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
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     1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
     1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
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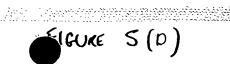
12/113

File: PAS23.DNA Range: 1 -Codon Table: Uni

5′

1554 al

Mode : Normal



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ATG	GGA 	TGG	AGC														
М	G	W	S	С	1	Ι	L	F	L	V	Α	Т	Α	Т	G	V	Н
		63			72			81			90			99			108
TCC	CAG		CAG	СТG	GTG				GCA	GAG		AAA	AAG	ССТ	GGG	GCC	TCA
					 V						- 	 v	 ĸ				s
S	Q	V	Q	L	V	Q	5	G	A	E	V	IX.		L	J	71	J
		117			126			135			144			153	maa		162
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT		TAC	1GG		GAG
V	K	V	s	С	K	A	s	G	Y	T	F	S	Α	Y	W	I	E
		171			180			189			198			207			216
TGG	GTG		CAG	GCT	CCA										АТТ	тта	
					 P										 I	 L	 Р
W	٧	R	Q	A	Р	G	V	G	ь	£	**	٧	G		-		-
		225			234		_	243			252			261	202	CMC.	270
GGA	AGT	AAT	TAA	TCT	AGA	TAC	TAA	GAG	AAG	TTC	AAG	GGC	CGA			GTC	ACT
G	s	N	N	S	R	Y	N	Е	K	F	K	G	R	V	Υ	V	т
		279	i		288			297			306			315			324
AGA	GAC			ACA	AAC		GCC			GAG						TCT	GAG
					 N						 L	 S	 S	 L	 R	 S	 E
К	D	Т	S	1	1/4	1	A	1	11	L			5	٦			
		333	•													CCT	378
GAC	ACA	GCC	GTC	TAT	TAC	TG1	· GCA	AGA		TAC	, GAC						
D	T	Α	V	Y	Y	С	A	R	S	Y	D	F	Α	W	F	A	Y
		381	7		396	;		405	.		414	1		423	.		432
TGG	GGG															CCA	TCG
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W	G	Q	G	Т	ъ	V	1	v	3		••	J	_				
		44			450		- m/-			2 00			2 GG(471		: GC(486 CTG
GTC																	
V	F	P	L	A	P	S	S	K	S	Т	S	G	G	Т	A	Α.	L
		49	5		50	4		513	3		52	2		53	1		540
GG	C TG			C AA			с тт	C CC	C GA			G AC	G GT	G TC	G TG0	S AAG	C TCA
 G	- - -		 . w		– – – D	 Y		 P				 Т	 V	<i>-</i> S	W	 N	 S
G	C	1.	. v		. 5		٠										
00	c cc	54		C AC	55		C CA			ר רר			ር ርጥ	58 a ca		с тс	594 A GGA
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- 1 -

621 630 603 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG --- --- --- --- --- --- --- --- --- --- --- --- ---Y S L S S V V T V P S S S L G T Q 684 693 675 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 720 729 738 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT E P K S C D K T H T C P P C P A P 792 801 783 774 GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG E G S G G L K I A A F N I Q T F G E 828 837 846 855 819 ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC --- --- --- --- --- --- --- --- --- --- --- --- --- ---T K M S N A T L V S Y I V Q I L S R 882 891 900 909 873 TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG Y D I A L V Q E V R D S H L T A V G 945 954 963 972 927 936 AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---K L L D N L N Q D A P D T Y H Y V V 999 1008 1017 981 990 AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG S E P L G R N S Y K E R Y L F V 1035 1044 1053 1062 1071 CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC ___ ___ 1098 1107 1116 1125 1134 TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG C G N D T F N R E P A I V R F F S R 1143 1152 1161 1170 1179 TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC F T E V R E F A I V P L H A A P G D 1197 1206 1215 1224 1233 1242 El Martin Charles

GCA GTA GCC GAC GAC GCT CTC TAT GAC GTC TAC CTG GTC CAA GAG AAA ___ ___ ___ A V A E I D A L Y D V Y L D V Q E K 1269 1278 1287 1296 1260 1251 TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT G L E D V M L M G D F N A G C S Y 1305 1314 1323 1332 1341 1350 GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---V R P S Q W S S I R L W T S P T F Q 1368 1377 1386 1395 1404 1359 TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT $\begin{smallmatrix} W & L & I & P & D & S & A & D & T & T & A & T & P & T & H & C & A & Y \\ \end{smallmatrix}$ 1413 1422 1431 1440 1449 1458 GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG 1503 1512 1485 1494 1467 1476 GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA ___ ___ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ 1530 1539 1548 GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' A I S D H Y P V E V M L K *

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ACCESSION
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KEYWORDS
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            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
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            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
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  MEDLINE
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                                   446 q
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BASE COUNT
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L> NLS

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LOCUS
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ACCESSION
KEYWORDS
CURCE
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                                  447 G
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Figure 6(c)

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     fraq
                     /note="1 to 78 of 102linker [Split]"
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                                           311 T
                         478 C
BASE COUNT
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      481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
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      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
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     1021 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
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     1141 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
     1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
     1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG
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     1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
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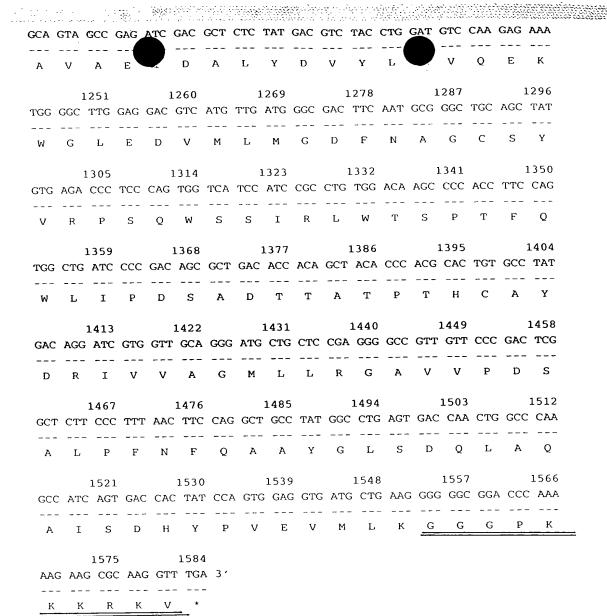
File: PAS27.DNA Range: 1 - 584 Codon Table: Universal

Mode : Normal



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621 630 CTC TAC TCC CTC AGC GTG GTG ACC GTG CCC TCC AGC TTG GGC ACC CAG 639 --- --- --- --- --- --- --- --- --- --- --- --- ---L Y S L S S V V T V P S S S L G T Q 693 684 666 675 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 747 720 729 738 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT E P K S C D K T H T C P P C 783 792 801 774 765 GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG E G S G G L K I A A F N I Q T F G E 855 819 828 837 846 ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC --- --- --- --- --- --- --- --- --- --- --- --- --- ---T K M S N A T L V S Y I V Q I L S R 900 909 882 891 TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG --- --- --- --- --- --- --- --- --- --- --- --- --- ---Y D I A L V Q E V R D S H L T A V G 945 954 936 AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC --- --- --- --- --- --- --- --- --- --- --- --- ---K L L D N L N Q D A P D T Y H Y V V 1017 1026 1008 999 990 981 AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG S E P L G R N S Y K E R Y L F V 1071 1044 1053 1062 CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC 1098 1107 1116 1125 1134 TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG T F N R E P A I V R F F S R 1152 1161 1170 1179 1143 TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC 1197 1206 1215 1224 1233 1242



(A) pAS34

2196 bp 2196 bp DNA 2196 bp 14-AUG-1998 PAS34.DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse construct 34 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) REFERENCE VERHOEYEN ET AL **AUTHORS** TITLE CONSTRUCTION OF RESHAPED HMFG1 etc IMMUNOL. (1993):78, 364-370 JOURNAL Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS79 and AS80 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** Note SITES 501 a 677 c 607 q 411 t BASE COUNT ? ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG 1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG 1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG 1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG 1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG 1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC 1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC 1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC 1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC 1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC 1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT 2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG 2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC 2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

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File: PAS34.DNA Range: 1 - 2196 Mode: Normal Codon Table: Uni



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ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA ___ --- --- --- --- --- --- ---V N H K P S N T K 729 738 747 720 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT PKSCDKTHTCPPCPAP 774 783 792 801 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC E L L G G P S V F L F P P K P K D T 855 837 846 828 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC 882 900 909 891 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT D P E V K F N W Y V D G V E V H N 945 954 963 936 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC --- --- --- --- --- --- --- --- --- --- --- --- ---K T K P R E E Q Y N S T Y R V V S 999 1017 1008 990 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---V L T V L H Q D W L N G K E Y K C K 1035 1044 1053 1062 1071 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1098 1107 1116 1125 1089 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1179 1170 1143 1152 1161 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC $\begin{smallmatrix} T & K & N & Q & V & S & L & T & C & L & V & K & G & F \end{smallmatrix}$ 1215 1224 1233 1206 1197 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG P E N N Y K T T I A V E W E S N G Q 1287 1278 1269 1251 1260 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG P P V L D S D G S F F L Y S K L T V 1305 1314 1323 1332 1341 1350 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

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G GGT AAA GGG ___ __ --- --- --- --- --- --- ---A L H N H Y T Q K S L S L S P G K G 1413 1422 1431 1440 1449 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---S G G L K I A A F N I Q T F G E T K 1467 1476 1485 1494 1503 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ___ ___ --- --- --- --- --- ---M S N A T L V S Y I V Q I L S R Y D 1548 1557 1539 1530 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG A L V Q E V R D S H L T A V G K L 1611 1584 1593 1602 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG L D N L N Q D A P D T Y H Y V V S 1665 1656 1647 1638 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC N S Y K E R Y L F V Y R PLGR 1719 1728 1701 1710 1692 1683 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---Y Y Y D D G C E P C G S A V D S 1764 1773 1782 1746 1755 1737 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA ___ ___ ___ N D T F N R E P A I V R F F S R F T 1791 1800 1809 1818 1827 1836 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA E V R E F A I V P L H A A P G D A V 1854 1863 1872 1881 1845 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---A E I D A L Y D V Y L D V Q E K W G 1935 1926 1917 1908 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA E D V M L M G D F N A G C S 1989 1980 1953 1962 1971 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---PSQWSSIRLWTSPTFQWL 2034 2043 2025 2016 2007 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG --- --- --- --- --- --- --- --- --- --- --- --- --- ---1 P D S A D T T A T P T H C A Y D R



(A) **pAS35**

2193 bp 2193 bp DNA PAS35.DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse construct 35 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G) DEFINITION REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 **JOURNAL** Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS81 and AS82 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** In 17.12.1 residue 1398 is A > G (silent K to K mutation) **FEATURES** Note SITES BASE COUNT 500 a 677 c 606 q 410 t ? ORIGIN

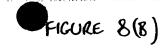
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGAAgGG GAGCGGCGGC CTGAAGATCG CAGCCTTCAA CATCCAGACA 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT 1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA

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File: PAS35.DNA Range: 1 -Codon Table: Universal

5,

Mode : Normal



ATG (GGA	9 TGG	a B AG	SC I	GT A	18 ATC <i>F</i>		СТС		TTG	GT		36 CA	ACA	GСТ	45 ACA		GT (GTC	54 CAC
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TCC	CAG	6 I	3 G C#	AG (CTG (72 GTG (CAG	тст		GCA	GA	.G C	90 GTG	AAA	AAG	99 CC1		GG '	GCC	108 TCA
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GTG	aag	11°	7 G T	cc '	TGC .	126 AAG	GCT	тст	135 GGC	TAC	AC		144 ITC	AGT	GCC	153 TAC		'GG	ATA	162 GAG
v		v		s	C	K	A	s	G	Y	r	r	F	s	Α	Y		W	1	E
TGG	GTG	17 CG	1 С С	AG	GCT	180 CCA	GGA	AAG	189 GGC	СТС	: G <i>I</i>		198 TGG	GTC	GGA	20°		\TT	тта	216 CCT
	v	 R		Q	Α	P	G	к	G	L	I	Ε	W	v	G	E		I	L	Ρ.
GGA	AGT	22 AA	5 .T A	AТ	TCT	234 AGA	TAC	AAT	243 GAG		; T		252 AAG	GGC	CGA	26 GT		ACA	GTC	270 ACT
G	s	N	1 -	N	s	R	Y	N	Е	K		F	К	G	R	V		Т	v	т
AGA	GAC	27 2 AC	79 CA T	rcc	ACA		ACA	GCC	297 TAC		G G	AG	306 CTC		: AGC	31 C CT		AGG	TCT	324 GAG
 R	D		 r	s	Т	N	т	A	Y	M		E	L	s	s	L	,	R	s	E
GAC	: AC	3: 4 G	33 CC (GTC	тат	342 TAC	TGT	GCA	351 AGA	TC	ст	`AC	360 GAC		r GC(36 TO		ТТТ 	GCT	378 TAC
- D	т		 A	v	Y	Y	С	Α	R	S		Y	D	F	A	V	V	F	Α	Y
TGG	G GG	3 C C	87 AA -	GGG	ACT	396 CTG	GTC	: ACA	405 A GTG		С I		414 GCC		C AC		23 AG	GGC	CCF	432 TCG
W	G		Q	G	Т	L	V	Т	v	S	;	S	Α	S	Т	1	K	G	Р	s
GTO	C TT	c c	41 CCC	CTG	GCA	450 CCC	TCC	C TC	45 C AA	G AC	SC A	ACC	468 TC				77 CA	GCC	GCC	486 C CTG
v	 F		P	L	A	P	S	s	к	5	5	Т	s	G	G	;	Т	Α	A	L
GG	C TC	C C			C AAC		TA		c cc	C G								TG	G AA	540 C TCA
G	- - -		L	v	К	D	Y	F	F)						7	S	W	N	S
GG	C G	~C (549 CTG	AC	C AG	55 C GG	C GT	G CA	C AC	C T	TC	CCC	G GC	T GI	nc ch	ra c	85 AG	TC	C TC	594 A GGA
G		V 	L	Т	 S	G	 V		1	r	F	P	A	, ,	/ 1	L	Q	S	S	G
CI	C T	AC	603 TCC	CT	C AG	61 C A G	C GI	'G GT	rg Ac	21 CC G	TG 	CC	63 C TC	C A	GC A	GC 1	539 rtg	GG	C AC	648 CC CAG
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ACC TAC ATC TGC CC GTG AAT CAC AAG CCC AGC AAC ACC ATCGTG GAC AAG AAA --- --- --- --- --- --- ---N V N H K P S N T K V D K K T Y I C 729 738 747 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T C P P C P A P 792 774 801 765 783 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC E L L G G P S V F L F P P K P K D 837 846 855 828 819 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC 909 882 891 900 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT $\begin{smallmatrix} E & D & P & E & V & K & F & N & W & Y & V & D & G & V & E & V & H & N \end{smallmatrix}$ 954 963 927 936 945 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC A K T K P R E E Q Y N S T Y R V V S 1017 990 999 1008 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG 1071 1053 1062 1035 1044 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1116 1125 1107 1098 1089 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1143 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC 1215 1224 1233 1242 1206 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG --- --- --- --- --- --- --- --- --- ---A V E W E S N G Q P E N N Y K T T 1278 1287 1260 1269 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG P P V L D S D G S F F L Y 1323 1332 1341 1314 1305 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG

1359 1368 1377 1386 1395 1404
GCT CTG CAC AAC TAC ACG CAG AAG AGC CTC TCC CTG TC A L H N H Y T Q K S L S L S P K G 1413 1422 1431 1440 1449 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG --- --- --- --- --- --- --- --- --- ---G G L K I A A F N I Q T F G E T K M 1467 1476 1485 1494 1503 TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC --- --- --- --- --- --- ---ATLVSYIVQILSRYDI 1566 1548 1557 1539 1530 1521 GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG L V Q E V R D S H L T A V G K L L 1602 1611 1584 1593 GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA Y H Y V V S E P D N L N Q D A P D T 1656 1665 1638 1647 1629 CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---L F V Y R P D Q L G R N S Y K E R Y 1710 1719 1728 1701 1692 GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC --- --- --- --- --- --- --- --- --- --- --- --- ---S A V D S Y Y Y D D G C E P C G N 1755 1764 1773 1746 GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---D T F N R E P A I V R F F S R F T E 1827 1836 1791 1800 1809 1818 GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC V R E F A I V P L H A A P G D A V A 1854 1863 1872 1881 GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG E I D A L Y D V Y L D V Q E K W G L 1935 1926 1917 1908 GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC L M G D F N A G C S E D V M 1980 1989 1953 1962 1971 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC --- --- --- --- --- --- --- --- --- --- --- --- ---Q W S S I R L W T S P T F Q W L I 2034 2043 2052 2025 2016 CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---P D S A D T T A T P T H C A Y D R I

2061 2070 2079 2088 2097 2106

GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC

V V A G M L L R G A V V P D S A L P

2115 2124 2133 2142 2151 2160

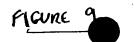
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT

F N F Q A A Y G L S D Q L A Q A I S

2169 2178 2187

GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

D H Y P V E V M L K *



(A) pAS36

DNA 14-AUG-1998 2190 bp 2190 bp LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse - construct 36 DEFINITION Clone 18.24.1 with residue 1392 T > C DEFINITION REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 **JOURNAL** Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS83 and AS84 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** Residue 1392 T > C silent S to S mutation FEATURES SITES Note 605 g 409 t 678 c 498 a BASE COUNT

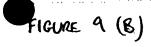
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT 1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC 1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG 1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT 1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC 1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC 2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

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ORIGIN

File: PAS36.DNA
Range: 1 - 2190
Codon Table: Universal

Mode : Normal



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		6	3			72 GTG	CAG	TCT	81 GGG		A G	AG (90 GTG	AAA	AAG	99 CC		GG	GCC	108 TCA
 S	 Q	 V			 L	 V	 Q	 S	 G	 A		 E	 V	- K	 K	P		G	Α	s
		11 GT	7 G 1	rcc	TGC	126 AAG	GCT	TCT	135 GGC	TA	C A		144 TTC	AGT	GCC	15 TA		'GG	ATA	162 GAG
 v	 к			s		 K	 A	- - -	 G			т	 F	s	Α	Y		W	I	E
TGG	GTY	17 5 CC	/1 GC (CAG	GCT	180 CCA	GGA	AAC	189 GGG	e C1	rc (198 TGG	GTC	GGA	20 GA		ATT	тта	216 CCT
 W	v	 F	∙ ₹	Q	 A	 P	G	К	G		 L	E	W	v	G	E	:	I	L	P
GGA	. AGʻ	22 r A	25 AT	ДДÝ	TCT	234 AGA	TAC	C AA'	24 r ga		AG '	TTC	252 AAG	GGC	: CG	26 GT		ACA	GTC	270 ACT
G	s		- - N	 N	s	R	Y	N	 E		ĸ	F	K	G	R	,	,	T	V	Т
AG <i>A</i>	. GA	2 C A	79 CA	TCC	AC#	288 AAC	B C AC	A GC	29 C TA	7 C A	TG	GAG	306 CTC		AG(31 C C1		AGG	TCT	324 GAG
R			 T	s	T	N	Т	 A	 Y	- -	M	E	L	s	s	1	L	R	s	E
GAG	C AC	3 :A G	33 CC	GTC	TA'	343 r TA	2 C TG	т gc	35 A AG	1 3A T	CC		360 GAC		r gc		69 GG	TTT	GCT	378 TAC
D	 1	•	A	V	Y	Y	С	A	. F	۲	s	Y	D	F	A	,	W	F	Α	Y
ТG	G GC	SC C	87 CAA	GGC	G AC	39 T CT	6 G GT 	C AC	40 CA G)5 rc 1	rcc	TCA	414 GCC	TC	C AC		23 AG 	GGC	CC2	432 A TCC
W	(3	Q	G	Т	L	V	, ;	r v	J	s	S	Α	S	Т	•	K	G	P	S
GT	С Т	rc (441 CCC	СТ	G GC		C TO		4°		AGC	ACC	468 TC'	r gg	G GG	C A	77 CA	GC0	G GC	480 C CTC
v		F	P	L	4	. F	> 5	5	S	K	s	Т					Т	A	A	L
		GC		GT	C AF		AC T	AC T		13 CC	GAA	CC	G GT	G AC	g G		531 rcg		G AA	54 C TC
		C	L	V				Y		P			V	1	י י	J	S	W	N	ı s
G	GC C	CC		AC	CC AG	5! GC G(58 GC G	TG C	AC A	67 ACC	ттс	. cc	G GC	T G	rc c	AT	585 CAG	TC	с тс	59 CA GG
- (G	Α	L			s ·						F			V	L	Q	S		s c
С	TC '	ľAC	60: TC	3 C C1	rc A	6 GC A			TG A	521 ACC	GTO	G CC	63 CC TC	CC A	GC A	GC	639 TTC	GG	SC AC	64 CC C7
-	L.	Y	s	1	 L	S									S					r (
			65	7		6	666			675			6	84			69	3		7

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG AAA TYICNVNHKPSNTKVDKK 738 747 720 729 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT P P C P A P 765 792 801 774 783 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC 855 837 846 828 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC S R T P E V T C V V V D V S H 909 891 900 882 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT D P E V K F N W Y V D G V E V H N 945 954 963 936 927 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC T Y R V V S 1017 999 1008 990 981 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG ___ ___ ___ L H Q D W L N G K E Y K C K 1053 1062 1071 1080 1044 1035 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---V S N K A L P A P I E K T I S K A K 1098 1107 1116 1125 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1179 1170 1143 1152 1161 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC K N Q V S L T C L V K G F Y P 1233 1206 1215 1224 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG P E N N A V E W E S N G Q 1278 1287 1269 1260 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG ___ __ __ 1323 1332 1341 1350 1314 1.305 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

1377 1386 1368 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC A L H N H Y T Q K S L S L S P G S G 1413 1422 1431 1440 1449 GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC G L K I A A F N I Q T F G E T K M S 1467 1476 1485 1494 1503 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC N A T L V S Y I V Q I L S R Y D I A 1557 1539 1548 1530 CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC V Q E V R D S H L T A V G K L L D 1620 1593 1602 1611 1584 AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG 1656 1665 1647 1638 GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG 1719 1701 1710 1692 1683 TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC Y D D G C E P C G N D 1755 1764 1773 1782 1737 1746 ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG GTC $\begin{smallmatrix} T & F & N & R & E & P & A & I & V & R & F & F & S & R & F & T & E & V \end{smallmatrix}$ 1800 1809 1818 1827 AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG R E F A I V P L H A A P G D A V A E 1872 1881 1845 1854 1863 ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG D A L Y D V Y L D V Q E K W G L E 1908 1917 1926 1935 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC D V M L M G D F N A G C S Y V R P S 1989 1971 1980 1962 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC 2025 2034 2043 2052 2016 GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

2061 2070 2079 2088 2097 2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT

V A G M L L R G A GGT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC

AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC

N F Q A A Y G L S D Q L A Q A I S D

2169 2178 2187

CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

H Y P V E V M L K *



511 a

?

683 c

(A) pAS37

2196 bp 2196 bp DNA 2226 bp PAS37.DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse construct 37 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) plus NLS DEFINITION REFERENCE VERHOEYEN ET AL **AUTHORS** TITLE CONSTRUCTION OF RESHAPED HMFG1 etc IMMUNOL. (1993):78, 364-370 **JOURNAL** Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS79 and AS80 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES FEATURES** Residue 963 is G > T leading to silent mutation in all clones SITES Note

619 q

413 t

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGGGTAA AGCGAGCCGC GGCCTGAAGA TCGCAGCCTT CAACATCCAG 1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG 1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG 1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG 1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG 1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC 1741 AACCGAGAGC CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC 1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC 1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC 1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC 1981 CCCACCTTCC AGTGGCTGAT CCCCGACAGC GCTGACACCA CAGCTACACC CACGCACTGT 2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG 2101 GCTCTTCCCT TTAACTTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC 2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGGC GACCCAAAAA GAAGCGCAAG 2221 **GTTTGA**

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BASE COUNT

ORIGIN

L> NLS

File: PAS37.DNA Range: 1 - 2226 Codon Table: Universal

5′

Mode : Normal



ATG (GGA	9 TGG	AGC	TGT	18 ATC .	ATC (CTC '	27 TTC	TTG	GTA	36 GCA	ACA	GСТ	45 ACA	GGT	GTC	54 CAC
	 G				 1						Α_	Т	Α_		G	v	н
TCC			CAG	CTG	72 GTG	CAG	тст		GCA	GAG	90 GTG	AAA	AAG	99 CCT	GGG	GCC	108 TCA
s		v	Q	L	v	Q	s	G	Α	E	v	K	К	P	G	Α	S
GTG	AAG	117 GTG	TCC	TGC	126 AAG		тст	135 GGC		ACC	144 TTC	AGT	GCC	153 TAC	TGG	ATA	162 GAG
v	ĸ	v	s	С	K					т	F	s	A	Y	W	I	E
TGG	GTG	171 CGC	CAG	GCT	180 CCA	GGA	AAG	189 GGC	CTC	GAG	198 TGG		GGA	207 GAG	ATT	TTA	216 CCT
 W	v	R	Q	A	P	G	ĸ	G	L	E	W	v	G	E	r	L	P
GGA	AGT	225 AAT	ААТ	TCT	234 AGA	TAC	AAT			TTC	252 AAG	GGC	CGA	261 GTG		GTC	270 ACT
G	s	N	N	s	R				K	F	K		R	V	T	v	T
AGA	GAC	279 ACA	TCC	ACA	288 AAC	ACA	GCC	TAC	ATG	GAG	306 CTC	AGC	AGC	315 CTG		тст	324 GAG
 R	D	T	s	т	N	T	Α	Y	М	E			s	L	R	s	Е
GAC	ACA	333 GCC	GTC	TAT	342 TAC	TGT	GCA	351 AGA	TCC	TAC		TTT	GCC	369 TGG		GCT	378 TAC
D	Т	A	v	Y	Y	С	Α	R	s	Y	D	F	Α	W	F	Α	Y
TGG	GGC	387 CAA	GGG	ACT	396 CTG	GTC	ACA	405 GTC		TCA			C ACC	423 AAG		CCA	432 A TCG
W	G	Q	G	\mathbf{r}	L	v	Т	V	s	s	A	s	Т	K	G	P	S
			CTO		450 A CCC	TCC			AGC				G GGG	477 C ACA		G GCC	486 C CTG
v	F	P	L		P	s	s	К	s		S	G	G	Т	Α	Α	L
GGC	TG	49 C CT	5 G GT	C AAC	504 G GAC	TAC	TTC	513 C CCC	G GA	A CC	52: G GT	G AC	G GT	53: G TC		AA E	540 C TCA
G	C	L	v	К		Y	F		Е	Р	V	Т	V	S	W	N	S
		54 C CT	G AC			,		C AC	C TT		G GC		с ст -		G TC	C TC.	594 A GGA
G		L		s								. v	L	Q	S	s	G
CT(С ТА	60 C TC	с ст	C AG	61: C AG	C GT	G GT	G AC	C GT	G CC	63 C TC	C AG	C AG	63 C TT	G GG	C AC	648 C CAG
L					s s				v			5 .5			G	Т	` Q
		65	57		66	6		67	5		68	34		69	3		702

C GTG AAT CAC AAG CCC AGC AAC ACC AA GTG GAC AAG AAA ACC TAC ATC TGC T Y I C N V N H K P S N T K V D K K 747 720 729 738 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT H T C P P C P A P K S C Т D K 783 792 774 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC L L G G P S V F L F P P 837 846 855 828 819 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC 900 909 891 882 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT E D P E V K F N W Y V D G V E V 936 945 954 963 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC --- --- --- --- --- --- --- --- --- --- ---N S T Y R V V S E Q Y P R E 1008 1017 990 999 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K 1035 1044 1053 1062 1071 1080 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1107 1089 1098 1116 1125 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1152 1170 1179 1161 1143 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC T K N Q V S L T C L V K G F Y P 1215 1224 1233 1206 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG I A V E W E S N G Q P E N 1287 1260 1269 1278 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG --- --- --- --- --- --- --- --- --- --- --- --- ---D S D G S F F L Y S K L T V 1314 1323 1332 1341 1350 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG D K S R W Q Q G N V F S C S V M H E

1377 1386 1359 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG L H N H Y T Q K S L S L S P G K G 1458 1431 1440 1449 1422 AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG S G G L K I A A F N I Q T F G E T K 1494 1503 1476 1485 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC M S N A T L V S Y I V Q I L S R Y D 1548 1557 1539 1530 1521 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG --- --- --- --- --- --- --- --- --- --- --- --- --- ---I A L V Q E V R D S H L T A V G K L 1593 1602 1611 1620 1584 1575 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG --- --- --- --- --- --- --- --- --- --- --- --- --- ---L D N L N Q D A P D T Y H Y V V S E 1638 1647 1656 1665 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC --- --- --- --- --- --- --- --- --- --- --- --- ---1683 1692 1701 1710 1719 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG Q V S A V D S Y Y Y D D G C E P C G 1746 1755 1764 1773 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA N D T F N R E P A I V R F F S R F T 1827 1818 1809 1800 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA 1863 1872 1881 1854 1845 GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC ___ ___ ___ E I D A L Y D V Y L D V Q E K W G 1917 1926 1935 1908 1899 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA --- --- --- --- --- --- --- --- --- --- ---L E D V M L M G D F N A G C S Y V R 1953 1962 1971 1980 1989 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG PSQWSSIRLWTSPTFQWL 2016 2025 2034 2043 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG PDSADTTATPTHCAYDR

2061 2070 2079 2088 2697 2106 ATC GTG GTG GTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT I V V A G M L L R G A V V V P D S A L 2115 2160 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC P F N F Q A A Y G L S D Q L A Q A I 2160 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG S D H Y P V E V M L K G G G G G P K K K K



(A) <u>pAS38</u>

2223 bp 2193 bp DNA LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse construct 38 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS DEFINITION REFERENCE VERHOEYEN ET AL **AUTHORS** CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 **JOURNAL** Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS81 and AS82 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** In 17.12.1 residue 1398 is A > G (silent K to K mutation) **FEATURES** SITES Note 412 t 618 g 683 c BASE COUNT 510 a ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CTCCGAAq**GG GAGCGGCGGG** CTGAAGATCG CAGCCTTCAA CATCCAGACA 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTCACAG AGGTCAGGGA GTTTGCCATT 1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGGGGGGC CCAAAAAGAA GCGCAAGGTT

LOMES

2221 <u>TGA</u>

File: PAS38.DNA Range: 1 -Codon Table: Universal

5,

Mode : Normal



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		9			18	.	ama	27	mmc.	C T N	36	NC N	CCT	45 ACA	CCT	GTC	54 CAC
ATG (GGA 	TGG	AGC	TGT													
М	G	W	S	С	<u>I</u>	<u>I</u>	L	F	L	V	A	T	<u>A</u>	<u>T</u>	G	<u></u>	<u>H</u> _
TCC	CAG	63 GTG	CAG	CTG			TCT						AAG	99 CCT	GGG	GCC	108 TCA
 S	 Q	 V	 Q	 L		 Q	s	 G	Α	E	v	K	K	P	G	A	s
GTG	AAG	117 GTG	TCC	TGC	126 AAG	GCT	TCT	135 GGC	TAC	ACC	144 TTC	AGT	GCC	153 TAC	TGG	АТА	162 GAG
	 K	 V	 s				 s			 T			 A	- Y	 W		 E
		171			180			189			198			207 GAG	АТТ	тта	216 CCT
1GG																	
W	V	R	Q	A	P	G	K	G	L	E	W	V	G	Е	1	L	P
GGA	AGT	225 AAT	ААТ	TCT	234 AGA	TAC	ААТ	243 GAG	AAG	TTC	252 AAG	GGC	CGA	261 GTG	ACA	GTC	270 ACT
G	s	N	N	s	R	Y	N	E	K	F	К		R	v	T	V	Т
AGA	GAC	279 ACA	TCC	. ACA	288 . AAC	ACA	GCC	297 TAC		GAG	306 CTC		AGC	315 CTG	AGG	тст	324 GAG
 R	 D	 T	 S	 Т	 N	 T	 A	 Y	 M	 E	L	 S	 S	 L	 R	-	 E
К	D			•			••				200			369	ı		378
GAC	ACA	333 GCC	GTC	rat c	342 TAC		GCA	351 AGA		TAC					TTT	GCT	
D	т	A	v	Y	Y	C	Α	R	s	Y	D	F	Α	W	F	A	Y
TGG	GGC	38° CA/	7 A GG0	g ACI	396 CTC		C ACA	405 A GTC		TCA	414 A GC0		. ACC	423 : AAC	s GGC	CCA	432 TCG
 W	 G		- -	 Т	 L	 V	 Т	 V	 s	 S	·		T	 К		P	s
		44	1		450)		459	.	C ACC	46: C TC		G GGC	477 C AC		G GCC	486 : CTG
		- - -	- - -				- - -			- -							
V	F	P	L	A	Ь	5	5	K								••	
			G GT			C TA			C GA	A CC					G TG	G AAG	540 TCA
G		 L										Т		s	W	N	S
GGG	c gc	54 C CT		C AG	55 C GG		G CA	56 C AC		c cc	57 :G GC		C CT	58 A CA		C TC	594 4 GGA
				 r s								 V					
G	Α			. 5			11							63			648
CT	С ТА	06 TC TC)3 CC C1	rc ac	61 C AG	2 C GT	G GI	62 G AC		G CC	63 C TC		C AG	с тт	GS o	C AC	C CAG
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GTG AAT CAC AAG CCC AGC AAC ACC A ACC TAC ATC TGC --- --- --- --- --- --- ---I C.N V N H K P S N T K V D K K 747 720 729 738 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---P K S C D K T H T C P P C P A 783 792 801 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC E L L G G P S V F L F P P K P K D T 828 837 855 846 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GAC GTG AGC CAC --- --- --- --- --- --- --- ---L M I S R T P E V T C V V V D V S H 900 909 891 882 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT 963 954 945 936 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC A K T K P R E E Q Y N S T Y R V 1017 1008 999 990 981 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG V L T V L H Q D W L N G K E Y K C K 1062 1071 1053 1044 1035 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA V S N K A L P A P I E K T I S K A K 1098 1107 1116 1125 1134 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG --- --- --- --- --- --- --- --- --- --- --- ---G Q P R E P Q V Y T L P P S R D E L 1152 1161 1170 1179 1188 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC --- --- --- --- --- --- --- --- ---1233 1215 1224 1197 1206 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG A V E W E S N G Q P E N N Y K T T 1287 1278 1269 1260 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG PPVLDSDGSFFLYSKLTV 1341 1314 1323 1332 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG --- --- --- --- --- --- --- --- --- --- --- --- ---D K S R W Q Q G N V F S C S V M H E

1368 1377 1386 395 1359 . GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC ______ L S L S P K <u>G</u> A L H N H Y T Q K S 1449 1431 1440 1422 GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG GGLKIAAFNIQTFGETKM 1476 1485 1494 1503 TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC S N A T L V S Y I V Q I L S R Y D I 1557 1530 1539 1548 GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG 1575 1584 1593 1602 1611 GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA 1647 1656 1665 1674 1638 CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG ___ ___ ___ R N S Y K E R Y L F V Y R P D Q 1710 1719 1692 1701 1683 GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC S A V D S Y Y Y D D G C E P C G N 1764 1773 1746 1755 1737 GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG D T F N R E P A I V R F F 1827 1800 1809 1818 GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC --- --- --- --- --- --- --- --- --- --- --- --- ---A I V P L H A A P G D A V A 1854 1863 1872 1881 1890 GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG E I D A L Y D V Y L D V Q E K W G L ·1899 1908 1917 1926 1935 GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC --- --- ---E D V M L M G D F N A G C S Y V R P 1971 1980 1989 1953 1962 TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC S Q W S S I R L W T S P T F Q W L I 2016 2025 2034 2043 CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC PDSADTTATPTHCAYDRI

2070 2079 2088 2097 2061 GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC --- --- --- --- --- --- --- --- --- --- --- --- --- ---V V A G M L L R G A V V P D S A L P 2115 2124 2133 2142 2151 2160 TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT --- --- --- --- --- --- --- --- --- --- --- --- ---Y G L S D Q L A Q A I S 2187 2196 2205 2214 2178 2169 GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC --- --- --- --- --- --- --- --- --- --- --- --- --- ---D H Y P V E V M L K G G

2223 AAG GTT TGA 3' --- --- K V *



(4) pAS39

DNA 2220 bp 2190 bp LOCUS HUMANISED HMFG1 heavy chain fused to human DNAse - construct 39 DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS DEFINITION REFERENCE VERHOEYEN ET AL AUTHORS CONSTRUCTION OF RESHAPED HMFG1 etc TITLE IMMUNOL. (1993):78, 364-370 **JOURNAL** Human DNAse sequence is modified as a result of oligo assembly COMMENT (mhdnase.dna) The fusion was made using overlapping oligos AS83 and AS84 COMMENT AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A) **FEATURES** Residue 963 is G > T leading to silent mutation in all clones **FEATURES** Residue 1392 T > C silent S to S mutation **FEATURES** SITES Note 617 g 411 t 684 c 508 a BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC 781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC 901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC 961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG 1201 TGGGAGACA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC 1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC 1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT 1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC 1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG 1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG 1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG 1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA 1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT 1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC 1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG 1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC 1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT 2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT 2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC 2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

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File: PAS39.DNA Range: 1 -Codon Table: Universal

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Mode : Normal



ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CA M G W S C I I L F L V A T A T G V H G3 72 81 90 99 10 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCC S O V Q L V Q S G A E V K K P G A S GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GA V K V S C K A S G Y T F S A Y W I TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA C W V R Q A P G K G L E W V G E I L 225 234 243 252 261 22 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG GTC AAG GGC CGA GTG ACA GTC ACC M C C C C C C C C C C C C C C C C C
M G W S C I I L F L V A T A T G V I TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TC S O V Q L V Q S G A E V K K P G A S GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GA V K V S C K A S G Y T F S A Y W I <td< th=""></td<>
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCC S O V Q L V Q S G A E V K K P G A 117 126 135 144 153 16 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GA V K V S C K A S G Y T F S A Y W I TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA C W V R Q A P G K G L E W V G E I L 225 234 243 252 261 22 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA GTG AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA GTG AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACC TTC TTC TTC TTC TTC TTC TTC TTC TTC
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117 126 135 144 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GATA G
V K V S C K A S G Y T F S A Y W I 171 180 189 198 207 2 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA C W V R Q A P G K G L E W V G E I L 225 234 243 252 261 2 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC A
171 180 189 196 TGG GTC GGA GAG ATT TTA C TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA C W V R Q A P G K G L E W V G E I L 225 234 243 252 261 2 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC A
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225 234 243 252 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC A
GON 1101 1211 12
G S N N S R Y N E K F K G R V T V
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D T A V Y Y C A R S 1 D 1 1 1 2 2 3
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA
WGQGTLVTVSSASTKGP
441 450 459 468 477 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC
V F P L A P S S K S T S G G T A A
495 504 513 522 531 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC
G C L V K D Y F P E P V T V S W N
567 576 585
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA
G A L T S G V H T F P A V L Q S S
603 612 621 630 639 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC
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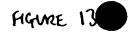
GTG AAT CAC AAG CCC AGC AAC ACC ATTG GAC AAG AAA ACC TAC ATC TG T Y I C N V N H K P S N T K V 738 747 729 711 720 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT V E P K S C D K T H T C P P C P A 792 783 801 774 765 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC ELLGGPSVFLFPPK 837 846 855 819 828 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC I S R T P E V T C V V V D V S H 891 900 909 882 873 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT 963 927 936 945 954 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC 1008 1017 999 981 990 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG N G K E Y K 1062 1071 1035 1044 1053 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA --- --- --- --- --- --- --- --- --- --- --- --- ---V S N K A L P A P I E K T I S K A K 1089 1098 1107 1116 1125 1134 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG G Q P R E P Q V Y T L P P S R D E L 1152 1161 1170 1179 1188 1143 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC --- --- --- --- --- --- --- --- --- --- --- --- ---N Q V S L T C L V K G F Y P S D 1215 1233 1197 1206 1224 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG A V E W E S N G Q P E N N Y K 1278 1287 1269 1260 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG F L Y S K D S D G S 1341 1323 1332 1314 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG ___ ___ ___

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1377 1386 68 1359 GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC GGG AGC GGC A L H N H Y T Q K S L S L S P G S G 1440 1449 1413 1422 1431 GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC --- --- --- --- --- --- --- --- --- ---G L K I A A F N I Q T F G E T K M S 1512 1467 1476 1485 1503 1494 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC N A T L V S Y I V Q I L S R Y D 1557 1548 1539 1530 1521 CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC L V Q E V R D S H L T A V G K L L D 1602 1611 1593 1584 1575 AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG L N Q D A P D T Y H Y V V S E P L 1638 1647 1665 1674 1656 GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG 1719 1710 1701 1692 1683 TCT GCG GTG GAC AGC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC --- --- --- --- --- --- --- --- --- --- --- --- --- ---S A V D S Y Y D D G C E P C G N D 1746 1755 1764 1773 ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA GAG GTC 1800 1809 1818 1827 AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG R E F A I V P L H A A P G D A V 1881 1872 1845 1854 1863 ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG I D A L Y D V Y L D V Q E K W G L E 1935 1926 1917 1908 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC 1989 1980 1971 1962 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC Q W S S I R L W T S P T F Q W L I P 2016 2025 2034 2043 2007 GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG --- --- --- --- --- --- --- --- --- ---D S A D T T A T P T H C A Y D R I V

GTT TGA 3'

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(A) <u>pAS101</u>

PRT PAS101.DNA 1548 bp mRNA LOCUS DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101) ACCESSION DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/fSOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE 467 c 430 q 308 t 343 a BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT 1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

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SOURCE
                     Location/Qualifiers
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53/113

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11

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ACCESSION
KEYWORDS
SOURCE
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      721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
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54/113

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5'

Mode : Normal



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GG	A A	GT	225 AAT	' AA	тт	'CT	234 AGA	TAC	: AA	T	243 GAG	AAG	тт	rc i	252 AAG		СС		261 GTG	ACA	A G		270 ACT
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AG	A G	SAC	279 AC) 4 T(CC A	ACA	288 AAC	ACA	A GO	CC '	297 TAC	TA	G GA	AG.	306 CTC	AG	C F	4GC	315 CTC	G AG	G T		324 GAG
 R		D	 Т	:		T		 T			 Y							s	L	R		s	E
GA	C P	AСА	33 GC	3 C G'	TC '	TAT	342 TAC	TG'	ГG	CA	351 AGA	TC	Э Т.	AC	360 GAC	тт	T (GCC			т (GCT	378 TAC
 D		 Т	 A					 C										Α	W	F		A	Y
TO	GG (GGC	38 CA	7 .A G	GG	ACT	396 CTC	5 G GT	C A	CA		TC	СТ	CA	GC	С Т(CC	ACC	42 AA	G GG	C (CCA	432 TCG
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G'	TC	TTO	44 C CC	cc c	CTG	GCA	45 CC	C TO	C T	rcc	AA	G AC	SC A	ACC	TC	тG	GG	GGC	: AC	7 A G		GCC	486 CTG
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		603			612			621			630	•		639			648
CTC	TAC	TCC	СТС	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
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T	Y	Ι	С	N	V	N	Н	K	P	S	N	Т	K	V	D	K	K
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GTT.	GAG	ccç	AAA	TCT	161	GAC	AAA	ACT	CAC	ACA	160			160	CCA	GCA	
v	E	P	ĸ	s	С	D	К	Т	н	т	С	P	P	С	P	Α	P
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		765			774			783			792			801			810
GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG
E	G	G	L	K	I	A	A	F	N	I	Q	${f T}$	F	G	E	Т	K
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ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	TTA	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC
M	S	N	Α	T	L	V	S	Y	I	V	Q	Ι	L	S	R	Y	D
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		873			882	~~~		891		0.0	900	1 Cm	000	909	000		918
ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG
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Ι	A	L	V	Q	E	V	R	D	S	п	ь	1	^	V	G	K	ப
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CTG	GAC		СТС	ТАА		GAC	GCA	CCA	GAC	ACC		CAC	TAC		GTC	AGT	
L	D	N	L	N	0	D	Α	P	D	т	Y	Н	Y	V	V	S	E
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V	V	3	Α.	V		5	•	•	•	D			•		-	Ŭ	Ŭ
		1089			1098	;		1107			1116			1125			1134
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N	D	T	F	N	R	E	P	Α	I	V	R	F	F	S	R	F	T
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GAG																	GTA
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 $\mathbf{pAS102}$

06-MAR-1995 mRNA PAS102.DNA 1566 bp LOCUS Humanised HMFG1 Fab'2 fused to human DNase I (pAS102) DEFINITION ACCESSION DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) (see Figure 2) Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** MEDLINE 91067672 345 a 469 c 440 q 312 t BASE COUNT ORIGIN

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1561 AAGTGA





SYN 23-MAR-2001 FDDNASE102 1566 BP SS-DNA FINITION ACCESSION **KEYWORDS** SOURCE 313 T 0 OTHER 440 G 468 C 345 A BASE COUNT ORIGIN 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC 10 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC tall. 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC 1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCGACAGC 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT

1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG

1561 GTGATGCTGA AGTGA

Figure 14 (C)

FDDNASE302 1575 BP SS-DNA SYN 29-AUG-2000 DEFINITION ACCESSION pAS302 KEYWORDS SOURCE Location/Qualifiers **FEATURES** 10..1575 frag /note="1 to 1566 of FdDNase102correct" 442 G 474 C 313 T BASE COUNT ORIGIN 1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA 1,0 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC 721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG 781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG 841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG 901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT 961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT 1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC 1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC 1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC 1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG 1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG

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1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
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Mode : Normal

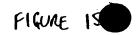
FIGURE 14 (D)

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M	G	W	s	С	r	I	L	F	L	V	Α	T	Α	Т	G	v	Н
	•	63			72			81			90			99			108
TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	ССТ	GGG	GCC	TCA
S	Q	v	Q	L	v	Q	S	G	Α	E	V	К	К	P	G	Α	S
		117			126			135			144			153			162
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
v	K	v	s	С	ĸ	A	s	G	Y	T	F	s	A	Y	W	I	E
		171			180	221		189		C N C	198	CTC	CCA	207	N TIVE	mm s	216
	GIG 		CAG	GCT			AAG									TTA	
W	v	R	Q	A	P	G	K	G	L	E	W	V	G	Е	I	L	P
		225			234			243			252			261			270
GGA	AGT	TAA	TAA	TCT	AGA	TAC	TAA	GAG	AAG	TTC	AAG 	GGC	CGA	GTG	ACA	GTC	ACT
G	S	N	N	s	R	Y	N	E	K	F	K	G	R	V	Т	V	Т
		279			288			297			306			315			324
AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
R	D	T	S	Т	N	Т	A	Y	M	E	L	S	S	L	R	S	Е
		333			342		~~*	351			360			369		COM	378
GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA			GAC					GCT	TAC
D	T	A	V	Y	Y	С	Α	R	s	Y	D	F	Α.	W	F	Α	Y
		387			396			405			414			423			432
TGG	G GGC	C CAA	GGC		CTG	GTC	ACA	GTC		TCF						CCA	
W	G	Q	G	Т	L	V	Т	V	S	S	A	S	Т	K	G	P	S
		44]			450			459			468			477			486
GTC	TTC	CCC	CTO	G GC	A CCC											GCC	
v	 F	P	L	A												А	
		495			50	•											540
GGG	TG(TAC										AAC	
G	С	L	V	К	D											N	S
000	0.00	54		0 10	558		- Cr	56		- cc			- Cm	585		~ m/~ a	59
GG(C AG0							. GC						
G	Λ	L	Т	S	G	V	H	Т	F	P	Α	V	L	Q	s	S	G

क्षेत्रके क्षेत्रके क्षेत्रके का विकास कर है। विकास का क्षेत्रक की का किस्सी का किस्सी का किस्सी का किस्सी का

CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA Y I C N V N H K P S N T K V D K K GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GAG TGC CCA CCG TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG PAPEGSGGLKIAAFNIQ ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG $\begin{smallmatrix} T & F & G & E & T & K & M & S & N & A & T & L & V & S & Y & I & V & Q \\ \end{smallmatrix}$ ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG I L S R Y D I A L V Q E V R D ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT Q D A 1017 1026 CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG 1044 1053 1062 1071 TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT V Y R P D Q V S A V D S Y Y Y D D 1098 1107 1116 GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG G C E P C G N D T F N R E P A I V R 1170 1179 1188 TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG $\begin{smallmatrix} F & & F & & S & & R & & F & & T & & E & & V & & R & & E & & F & & A & & I & & V & & P & & L & & A \\ \end{smallmatrix}$ 1197 1206 1215 1224 1233 1242

وأوجوا أورق والإنجاز والمرازي والمستحدد والمستحدة والمحادث والمستحدد والمستحدد والمستحدد والمستحدد والمستحدد والمستحدد والمستحد والمستحدد والمستحد والمستحدد والمستحد والمستحدد والمستحد والمستحدد والمستحد والمستحد والمستحدد والمستحدد والمستحدد والمستحدد والمستحدد وال A GTA GCC GAG ATC GAC GCT CTC TAT A P G D A V A E I D A L Y D V Y L D 1251 1260 1269 1278 1287 1296 GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG --- --- --- --- --- --- --- --- --- --- --- --- --- ---V Q E K W G L E D V M L M G D F N A 1314 1323 1332 1341 1305 GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC P S Q W S S I R L W T S 1368 1377 1386 1359 CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---P T F Q W L I P D S A D T T A T P T 1422 1431 1440 1449 1413 CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---H C A Y D R I V V A G M L L R G A V 1467 1476 1485 1494 1503 1512 GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC V P D S A L P F N F Q A A Y G L S D 1521 1530 1539 1548 1557 CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' Q L A Q A I S D H Y P V E V M L K *



(A) pAS103

06-MAR-1995 PRI 1560 bp mRNA PAS103.DNA LOCUS DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103) ACCESSION NID DNase I. KEYWORDS DNase I sequence is from assembled oligos (thus modified c/fSOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** MEDLINE 91067672 344 a 468 c 436 q 312 t BASE COUNT

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ORIGIN

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Figure 15 (B)

SYN 25-AUG-2000 FDDNASE103 1560 BP SS-DNA CCCUS FINITION CCESSION : KEYWORDS SOURCE Location/Qualifiers FEATURES join(1..>720,<793..1560) frag /note="1 to 1560 of PAS103.dna [Split]" 721..792 frag /note="1 to 72 of 103/107linker" join(721..>771,<772..792) frag /note="1 to 78 of 102linker [Split]" 0 OTHER 436 G 313 T BASE COUNT 467 C ORIGIN 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC $\mathbb{D} \oplus$ 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 7.0. 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA 901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC 1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG

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1561 CTGAAGTGA

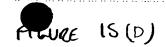
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Figure 15 (c)

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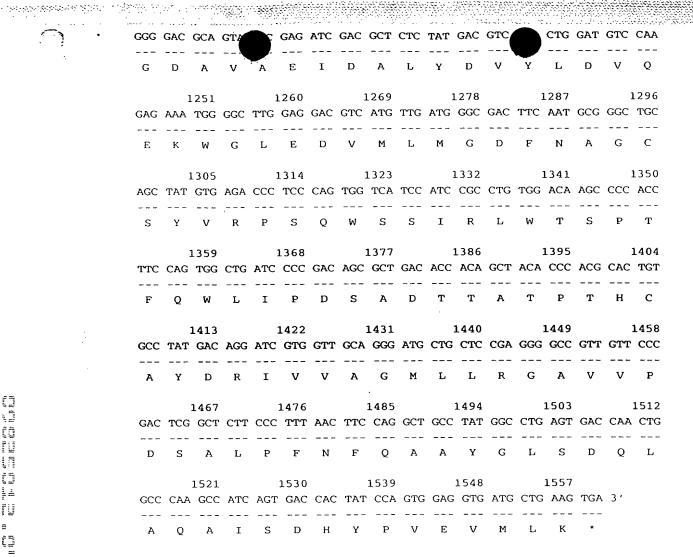
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Mode : Normal



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 M	G	 W	S	C	 I	 I	 L	 F	 L	 V	 A	- Т	 A	т	 G	v	н
		63			72			81			90			99			108
TCC	CAG	GTG	CAG	CTG	GTG	CAG	тст	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
S	Q	V	Q	L	V	Q	s	G	Α	Е	v	K	K	P	G	A	S
GTG	AAG	117 GTG	TCC	TGC	126 AAG		TCT	135 GGC	TAC	ACC	144 TTC	AGT	GCC	153 TAC		ATA	
	 К	 V	s				S	 G	 У	T	 F	s	A	Υ	W	I	E
TGG	GTG	171 CGC	CAG	GCT	180 CCA	GGA	AAG	189 GGC	CTC	GAG	198 TGG	GTC	GGA	207 GAG	ATT	тта	216 CCT
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W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	Ι	ה	r
001	N CIO	225	N N M	тст	234		አአጥ	243					CGA	261 GTG		GTC	270 ACT
GGA 	AGT	AAT	AAT		AGA												
G	S	N	N	S	Ŗ	Y	N	E	K	F	K	G	R	V	Т	V	T
		279			288			297			306			315			324
AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
R	D	Т	S	Т	N	Т	Α	Y	М	E	L	S	S	L	R	S	E
		333			342			351			360		000	369		CCM	378
GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC						
D	T	Α	V	Y	Y	С	Α	R	s	Y	D	F	A	W	F	Α	Y
		387			396			405			414			423			432
TGC	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	A GCC	TCC	ACC	AAG	GGC	CCA	TCG
W	G	Q	G	т Т	L	V	Т	v	s	s	А	S	Т	K	G	P	S
		441			450	1		459	,		468	₹		477	,		486
GTO	TTO			G GCA			TCC			ACC			GGC			GCC	
 V	 F	 P	· L	 A	 P	 S	 S	- -		т	 S	 G	. -	т	 А	A	 L
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GG	C TG	495 CTC		C AAC	504 G GAC		C TTC			A CC	522 G GT0		G GTO	531 TC0		S AAC	540 TCA
		- -					- ·										
G	С	L	V	K	D	Y	F	P	E	Ð	V	1	V	5	W	N	S
66	c cc	54		C 10	558		~ CA		7 - 11110				~ Cm;	589 CAC		ጉ ጥር፣	594 GGA
			- AC														
G	Α	I.,	T	S	G	V	Н	Т	F	Þ	Α	V	L	Q	S	S	G

630 621 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L Y S L S S V V T V P S S S L G T Q 684 693 675 657 666 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---T Y I C N V N H K P S N T K V D 738 747 720 729 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG V E P K S C D K T H T C C V E C P P 792 774 783 TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT --- --- --- --- --- --- --- --- --- --- --- --- ---A A F N I Q T F L K I C P A P E G G 855 846 837 828 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG --- --- --- --- --- --- --- --- --- --- --- --- ---900 909 891 882 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC --- --- --- --- --- --- --- --- --- --- --- --- --- ---I A L V Q E V R D S H L T A 963 945 954 936 927 GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC V G K L L D N L N Q D A P D T Y H Y 999 1008 1017 1026 990 981 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG --- --- --- --- --- --- --- --- --- --- --- --- --- ---V V S E P L G R N S Y K E R Y L F V 1062 1053 1071 1044 1035 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC Y R P D Q V S A V D S Y Y D D 1116 1125 1134 1107 1098 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC ___ ___ ___ E P C G N D T F N R E P A I V R F F 1152 1161 1170 1179 1188 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG --- --- --- --- --- --- --- --- --- --- --- --- ---S R F T E V R E F A I V P L H A A P 1197 1206 1215 1224 1233 1242





(f) pAS104

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Linker GR instead of GG (position 777)
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KEYWORDS
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            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
  AUTHORS
            Recombinant human DNase I reduces the viscosity of cystic fibrosis
  TITLE
            sputum
            Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
  JOURNAL
  MEDLINE
            91067672
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                346 a
                          468 c
BASE COUNT
ORIGIN
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Figure 16(B)



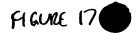
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TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA 	AAG	CCT	GGG	GCC	TCA
S	Q	v	Q	L	v	Q	S	G	Α	E	V	K	K	P	G	Α	s
		117			126			135			144			153			162
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
v	K	v	s	С	ĸ	A	s	G	Y	Ť	F	s	A	Y	W	I	E
		171			180			189			198			207			216
TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
W	v	R	Q	A	P	G	K	G	L	E	W	v	G	E	I	L	P
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GGA	AGT	raa	TAA	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
G ·	s	N	N	s	R	Y	N	E	K	F	K	G	R	V	Т	v	Т
		279			288			297			306			315			324
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R	D	т	S	Т	N	Т	Α	Y	М	E	L	S	S	L	R	S	E
		333			342			351			360			369			378
GAC	ACA	GC0	GTO	TAT	TAC	TGI	GCA	AGA	TCC	TAC	GAC	T TT	GCC	TGG		GCT	TAC
D	Т	Α	V	Y	Y	С	Α	R	S	Y	D	F.	Α	W	F	Α	Y
		38			396						414						432
TGC	GGG	CA.	A GGG	G ACT	r CTG	GT(C ACA	GTC	TCC	TCA	GCC	TCC	ACC	. AAG	GGC	CCA	TCG
W	G	Q	G	Т	L	V	Т	V	S	S	Α	S	Т	K	G	P	S
		44			450						468			477			486
GT(TT(C CC	C CT		A CCC						TC1		G GG(ACA	A GC0	G GCC	CTG
V	F	Р	L	A	P	S	S	K	S	Т	S	G	G	T .	A	Α	L
		49			504			513			522			533			540
GG	С ТG	C CT	G GT		G GAG		C TT(C GA2		G GTO			G TC0	G TG0 	G AA0	TCA
G	С	L	, v	K	D	Y	F	P	E	Р	V	Т	V	S	W	N	S
		54			55									58		o ~-	594
GG 	C GC	C CI	G AC		C GG				C TT		G GC' 						A GGA
G	A	. I	r	` s	G	V	Н	Т	F	p	Α	V	L	Q	S	S	G

621 630 639 603 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG ___ ___ ___ V V T V P S S S L G T Q y s L s s 675 684 693 666 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA T Y I C N V N H K P S N T K V D K K 729 738 747 711 720 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---792 801 774 783 765 TGC CCA GCA CCT GAA GGC AGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT --- --- --- --- --- --- --- --- --- --- --- --- --- ---C P A P E G R L K I A A F N I Q T F 837 846 855 828 819 GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG --- --- --- --- --- --- --- --- --- --- --- --- ---G E T K M S N A T L V S Y I V Q I L 909 900 873 882 891 AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC ___ ___ ___ S R Y D I A L V Q E V R D S H L T A 945 954 936 927 GTG GAG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC ___ ___ V E K L L D N L N Q D A P D T Y H Y 999 1008 1017 1026 990 981 GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG ___ ___ ___ R Y L F V Y K E 1062 1071 1044 1053 TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC 1098 1107 1116 1125 1134 1089 GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC --- --- --- --- --- --- --- --- --- --- --- --- ---P C G N D T F N R E P A I V R F F 1152 1161 1170 1179 1143 TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG S R F T E V R E F A I V P L H A A P 1197 1206 1215 1224 1233 1242 GGG GAC GCA GTA-GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA -- --- --- --- --- --- ---A E I D A L Y D V YLDVQ G D A V 1278 1287 1269 1251 1260 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC E K W G L E D V M L M G D F N A G C 1314 1323 1332 1341 1350 1305 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC ___ ___ S Y V R P S Q W S S I R L W T S P T 1368 1377 1386 1395 1359 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT --- --- --- --- --- --- --- --- --- --- --- --- ---F Q W L I P D S A D T T A T P T H C 1422 1431 1440 1449 1458 1413 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC --- --- --- --- --- --- --- --- --- --- --- --- ---1485 1494 1503 1476 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG 1521 1530 1539 1548 1557 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3' A Q A I S D H Y P V E V M L K \star



(A) pAS105

06-MAR-1995 PRI PAS105.DNA 1578 bp mRNA LOCUS Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS105) DEFINITION ACCESSION **KEYWORDS** DNase I. DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) Homo sapiens ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. **AUTHORS** Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE 353 a 473 c 442 g 310 t BASE COUNT ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT 1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG 1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA 1561 AAGAAGCGCA AGGTTTGA - NLS

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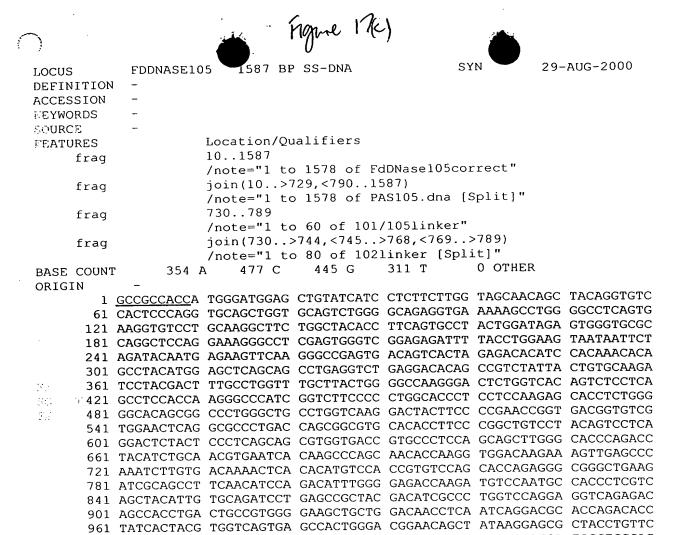
Figure 17(B)



SYN 25-AUG-2000 1578 BP SS-DNA FDDNASE105 CUS FINITION ACCESSION REYWORDS SOURCE Location/Qualifiers **FEATURES** join(1..>720,<781..1578) frag /note="1 to 1578 of PAS105.dna [Split]" frag /note="1 to 60 of 101/105linker" join(721..>735,<736..>759,<760..>780) frag /note="1 to 80 of 102linker [Split]" 443 G 311, T 471 C BASE COUNT ORIGIN 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC 121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA ø. 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC 501 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT 721 GACAAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC 781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT 841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG 901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC 961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG 1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG 1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC 1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC 1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG 1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC 1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA 1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT 1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG

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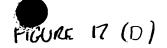
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1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCGGGGGA CGCAGTAGCC
1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
1261 GTCATGTTGA TGGGCGACTT CAATGCGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
1441 GGGGCCGTTG TTCCCGACTC GGCTCTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
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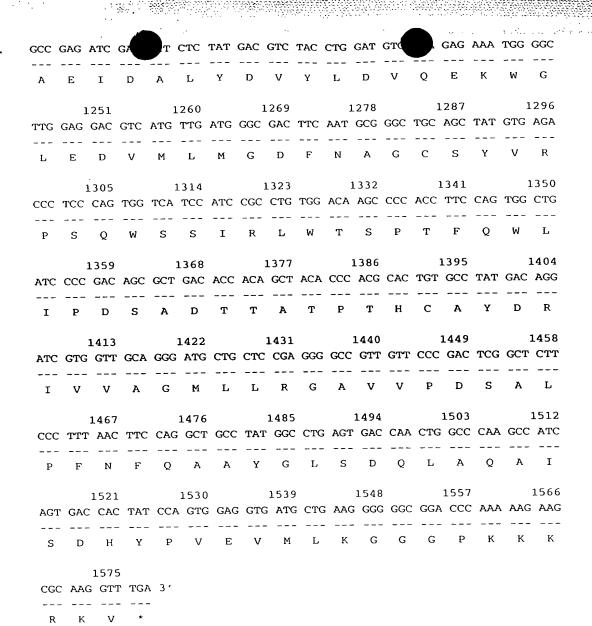
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Mode : Normal



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		63	3			72			81				90				99				80
TCC	CAG	GTO	G CA	AG (CTG	GTG	CAG	TCT	GGG	GC	CA C	GAG	GTG	AAA 	. A <i>l</i>	AG(CCT	GGG	GCC	T(CA
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G	GC G	CC (549 CTG	AC	C A	GC G	58 GC G	TG C	AC A	667 ACC	TT	c co	cg G	ст С	STC	СТ	A C	AG TO	CC T	CA	GGA
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630 639 612 621 603 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG --- --- --- --- --- --- --- --- --- --- --- --- ---Y S L S S V V T V P S S S L G T Q 693 684 666 675 657 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAA --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---T Y I C N. V N H K P S N T K V D K K 747 729 738 720 711 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT --- --- --- --- --- --- --- --- --- --- --- --- --- ---V E P K S C D K T H T C P P C P A P 801 792 783 774 765 GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---G G L K I A A F N I Q T F G E T K 846 855 828 837 819 ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC M S N A T L V S Y I V Q I L S R 900 891 873 882 ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG --- --- --- --- --- --- --- --- --- --- --- --- ---I A L V Q E V R D S H L T A V G K 963 945 954 936 CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG --- --- --- --- --- --- --- --- --- --- --- --- ---Y 1008 1017 990 999 981 CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---PLGRNSYKERYLFVYRPD 1062 1071 1080 1053 1044 1035 CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG $\begin{smallmatrix} Q & V & S & A & V & D & S & Y & Y & P & D & G & C & E & P & C & G \end{smallmatrix}$ 1098 1107 1116 1125 AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TCC CGG TTC ACA D T F N R E P A I V R F F S R F T 1143 1152 1161 1170 1179 1188 GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA ___ ___ ___ E V R E F A I V P L H A A P G D A V 1197 1206 1215 1224 1233



ORIGIN

11



/A) pAS106

06-MAR-1995 PRI 1596 bp mRNA Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS106) DEFINITION ACCESSION NID **KEYWORDS** DNase I. DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) ORGANISM Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE 475 c 452 q 314 t 355 a BASE COUNT

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-> NLS

Figure 12(B)

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***FINITION
: CCESSION
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421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCTACT CONSTRUCT CONSTRUCT AND 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
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      841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
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14

Figure 12(c)

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      361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
\mathcal{O}_{\Sigma}
     : 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCT CCTCCAAGAG CACCTCTGGG
\mathbb{A}_{+}^{+}
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KE
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Mode : Normal



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	 G	 W	 S	 C	 I	 I	 L	 F	 L	 V	 A	 Т	 A	 T	 G	v	 Н
maa	010	63	CAG	CTC	72	CAC	π∕·π	81	CCA	CAC	90 CTC		አልሮ	99 CCT	CCC	CCC	108 TCA
S	Q	V	Q	L	V	Q	S	G	Α	E	V	K	K	P	G	A	S
GTG	AAG	117 GTG	TCC	TGC	126 AAG		тст	135 GGC	TAC		144 TTC	AGT	GCC	153 TAC	TGG	ATA	162 GAG
 V	 К	 v	 s	 С	к	A	 S	 G	Y	 Т	 F	s	 A	Y	w		E
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	s	N	N	s	R	Y	N	 E	K	F	K	G	R	v	т	V	T
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D	Т	Α	V	Y	Y	С	Α	R	S	Y	D	F	А	W	F	Α	Y
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W	G	Q	G	Т	L	v	Т	v	S	s	Α	S	T	K	G	P	s
GTC	TTC	441 CCC	L C CTC	G GC#	450 4 CCC		rcc	459 AAG		: ACC	468 TCT		GGC	477 ACA		GCC	486 CTC
 V	 F	P	 L	A	P	s	s	. -	s	Т	s	G	G	Т	Α	Α	L
	- mai	49	5 G GT	~ **	504		~ mm/			CCC			CTC	531	_	: AAC	54 TC
)ئى)ى 				_ AA(. GAC		- -		. GAA								
G	С	L	V	K	D	Y	F	P	E	P	V	Т	V	S	W	N	S
GG	C GC	54 C CT	G AC			C GTO			C TTC			r GTC			G TCC		59 \ GG
 G		 L	 T									·		Q.			G

621 630 603 612 CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG L S S V V T V P S S S L G T Q 675 684 693 657 666 ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAA --- --- --- --- --- --- --- --- --- --- --- --- --- ---P S N T K V D н к 747 738 720 729 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG ___ ___ ___ ___ ___ ___ ___ E P K S C D K T H T C C V E C P P 792 801 774 783 TGC CCA GCA CCT GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG GGLKIA A F N I Q E G S 846 855 837 819 828 ACA TTT GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG E T K M S N A T L V S Y I V Q 900 909 873 882 891 ATC CTG AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG L S R Y D I A L V Q E V R D S H L 945 954 963 936 927 ACT GCC GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT T A V G K L L D N L N Q D A P D T Y 999 1008 1017 1026 990 CAC TAC GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG ___ ___ H Y V V S E P L G R N S Y K E R Y L 1062 1071 1044 1053 1035 TTC GTG TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT $F \quad V \quad Y \quad R \quad P \quad D \quad Q \quad V \quad S \quad A \quad V \quad D \quad S \quad Y \quad Y \quad Y$ 1116 1125 1098 1107 GGC TGC GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG ___ __ __ __ __ __ __ __ ___ ___ ___ ___ ___ ___ 1152 1161 1170 1179 1188 TTC TTC TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG F F S R F T E V R E F A I V P L H A 1224 1233 1242 1197 1206 1215

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11

FI CURE 19

(h) pAS107

06-MAR-1995 1590 bp PRI mRNA PAS107.DNA Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS107) DEFINITION ACCESSION NTD **KEYWORDS** DNase I sequence is from assembled oligos (thus modified c/f SOURCE MHDNASE1.dna) Homo sapiens ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L. AUTHORS Recombinant human DNase I reduces the viscosity of cystic fibrosis TITLE sputum Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990) **JOURNAL** 91067672 MEDLINE 474 c 448 q 314 t 354 a BASE COUNT ORIGIN

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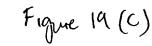
LONLS

Figure 19 (8)

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1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

17





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29-AUG-2000
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1.0CUS
UNFINITION
ACCESSION
MEYWORDS
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r.E
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      541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
      601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
      661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
      721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
      781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT
      841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
      901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
      961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
     1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
     1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
     1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
     1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
     1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
     1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
     1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG
     1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
     1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
```

1561 CTGAAGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA

File: PAS107.DNA
Range: 1 - 590
Codon Table: Universal

5'

Mode : Normal



ATG	CC	, m	9	ለርር	ጥርጥ	18 ATC	ra '	rc (CTC	27 T TC	тт	rg (ATE			.CA			15 CA (GGT	GTC		64 AC
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1CC	CA												-									_	
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GTG	AA	1 .G G	17 STG	TCC	TGC	12 : AA	6 G G	СТ	TCT	135 GGC			ACC		_	AGT			53 AC	TGG	ATA		62 AG
 V		 (v	 s	c			 A	s	G	-	Y	т	F	•	s	A		Y	W	I		E
TGG	G G	rg (171 CGC	CAG	GC:	18 r CC			AAG				GAG		-	GTC			07 AG	TTA	тт		16 CT
 W		· J	 R	 Q	 A	 F	- -	G		G		L	E	· -·	N	v	G	- -	E	I	L		P
GGA	A A	GТ	225 AAT	AA	r TC	23 T AC			RAA	24 GA		A AG	TTC		52 AG	GGC	CG.		e etg	ACA	GT		270 ACT
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			279			2	88		ccc	29 - Ta	•		GAG	_	-		: AG		315 CTG	AGG			324 GAG
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GA	C F	ACA	333 GC0		C TA	т т	AC	TGI	GC.	A A	3A	TCC	TA	c c	SAC	TT:	r GC	:C '	369 TGG	TT:	r GC		378 TAC
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~	CC	ጥርረ	49)5 CC C	:TC 7	AG	504 GAC	та	C T	rc c	13 CCC		ΑС		522 GT0	_	CG G		53 TC		GG A	AC	540 TCA
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G	GC	GC	54 C C'	19 rg <i>i</i>	ACC A	AGC	558 GGC		rg C	AC A	567 ACC	T1	rc c	CG	57 GC	т G	TC (СТА	58 . C7	G T	cc ′	rca -	594 GGA
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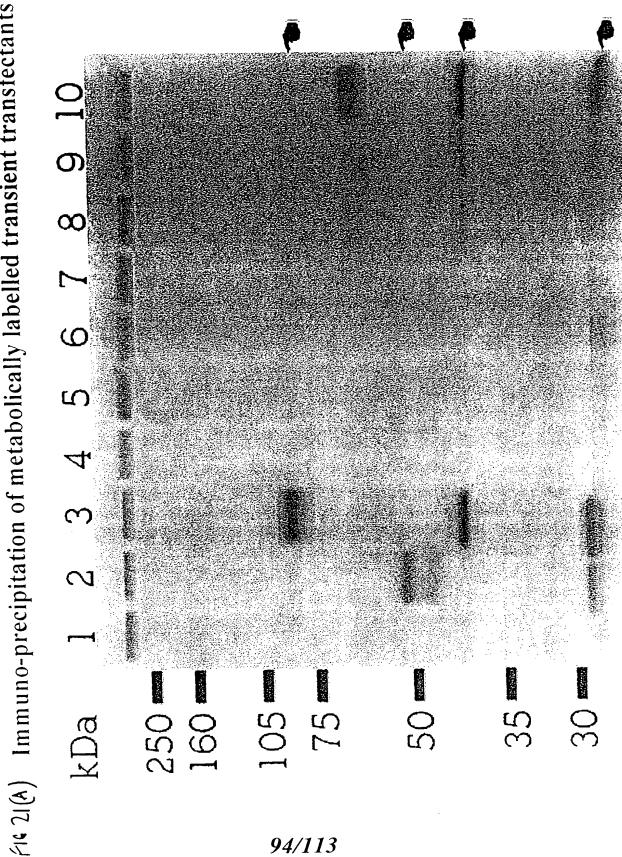
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CTC	TAC														GGC	ACC	
 L	 Y	- S	 L	 S	 S	 V	 V	T		 P	 S	 S	 S	 L	 G	 T	0
IJ	ı	3	ь	3	3	v	V	•	v	-	5	J		IJ	G	•	V
		657			666						684			693		•••	702
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
Т	Y	I	С	N	V	N	Н	K	P	S	N	Т	К	V	D	K	K
					700			300			720			747			25.6
GTT	GAG	711 CCC	AAA	TCT	720 TGT				CAC			TGT		747 GAG	TGC	CCA	756 CCG
V	E	P	K	S	С	D	K	Т	Н	Т	С	С	V	Е	С	P	P
		765			774			783			792			801			810
TGC	CCA	GCA	CCT	GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT
	 · P	 A	 P		 G	 G	 L	 K		 A	 A	 F	 N		 Q	 Т	 F
C	r	Α	E	L	G	G	п	10	•			•	14	•	v	•	•
		819			828			837			846			855	~~~		864
GGG	GAG	ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG
G	E	T	K	М	S	N	A	Т	L	v	s	Y	Ι	V	Q	Ι	L
		873			882			891			900			909			918
AGC	CGC	TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC
S	R	Y	D	I	A	L	v	Q	Е	V	R	D	S	Н	L	Т	А
GTG	GGG	927		СТС	936 GAC		ርፕር				954 GCA		GAC		TAT		972 TAC
V	G	K	L	L	D	N	L	N	Q	D	Α	P	D	Т	Y	Н	Y
		981			990			999			1008			1017			1026
GTG	GTC	AGT	GAG	CCA	CTG										CTG		GTG
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TAC															GAT		
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		1089															
GAG	CCC	TGC	GGC	AAC	GAC				CGA						AGG		TTC
Е	Р	С	G	N											R		F
		1143	3		1152	?		1161			1170)		1179			1188
TCC	CGC	TTC	C ACA	GAG	GTC	AGC		TT7			GTI		CTC	CAT	, ece	GCC	CCG
S	R	F	т	E	v	R							L L	Н	Α	A	P
		119	7		1206	5		1215	5		1224	١		1233	,		1242

GGG GAC GCA GTA GAC GCT CTC TAT GAC GTC CTG GAT GTC CAA G D A V A E I D A L Y D V Y L D V Q 1251 1260 1269 1278 1287 1296 GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC ___ ___ E K W G L E D V M L M G D F N A G C 1305 1314 1323 1332 1341 1350 AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC 1359 1368 1377 1386 1395 1404 TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT --- --- --- --- --- --- --- --- --- --- --- --- --- ---F Q W L I P D S A D T T A T P 1413 1422 1431 1440 1449 GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC --- --- --- --- --- --- --- --- --- --- --- --- --- ---1467 1476 1485 1494 1503 1512 GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG ___ ___ __ D S A L P F N F Q A A Y G L S D Q L 1530 1539 1548 1557 1566 1521 GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---A Q A I S D H Y P V E V M L K G G G 1575 1584 CCC AAA AAG AAG CGC AAG GTT TGA 3' ___ __ __ __ P K K K R K V *

FIG 20

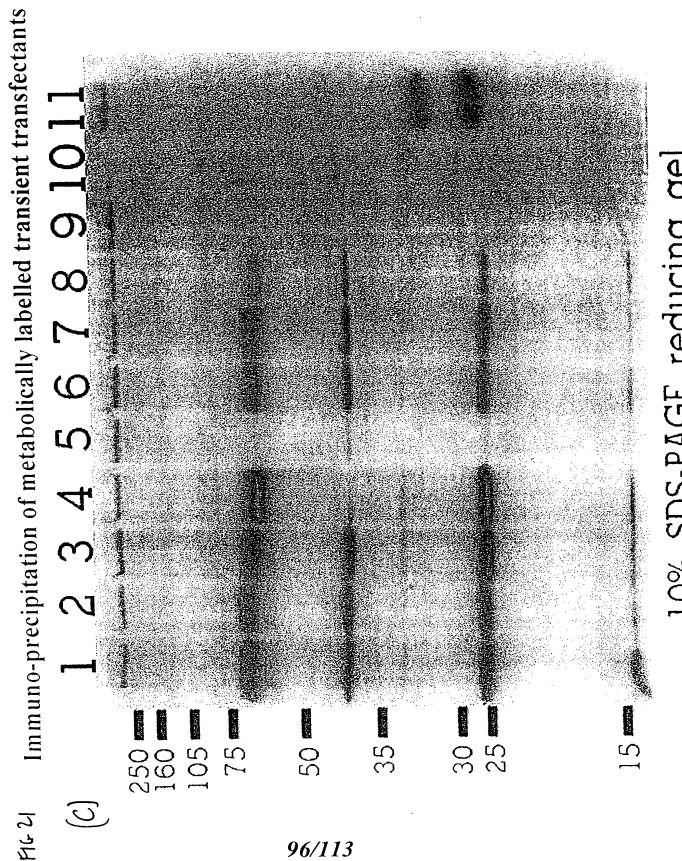
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14 21(A) Immuno-precipitation of metabolically labelled transient transfectants

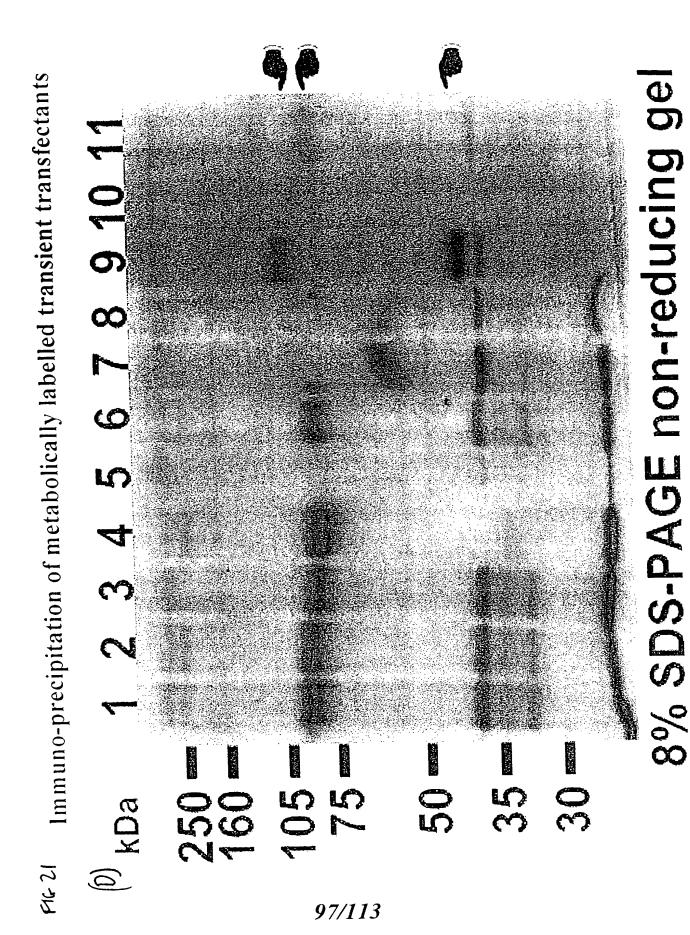


8% SDS-PAGE reducing gel

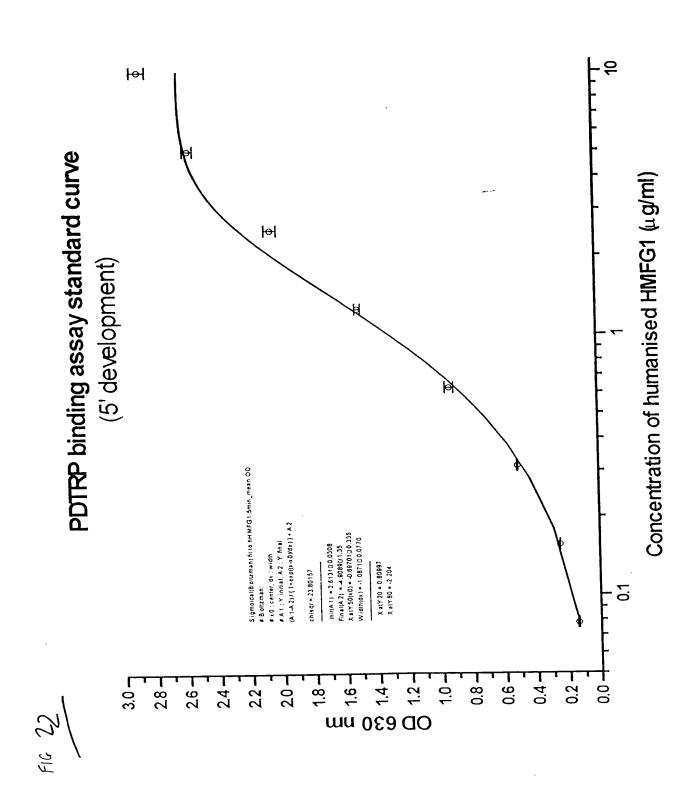
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10% SDS-PAGE reducing gel



:



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Corrected bovine DNase I standard curves at various time points

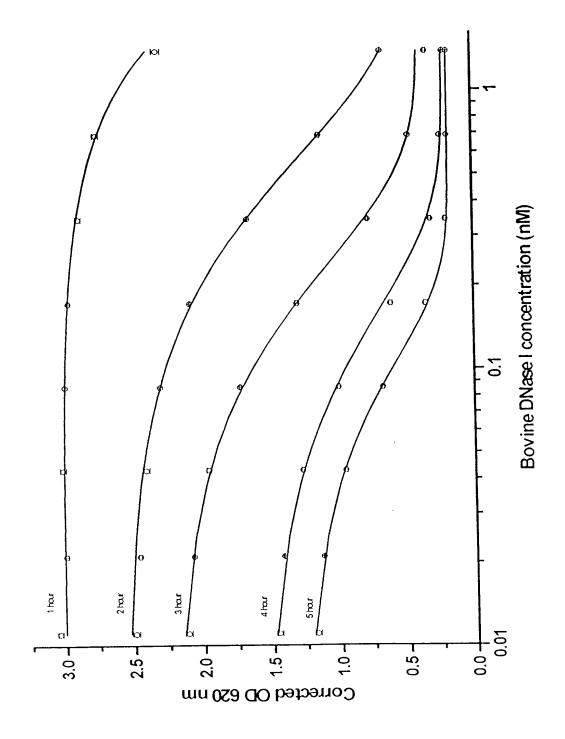
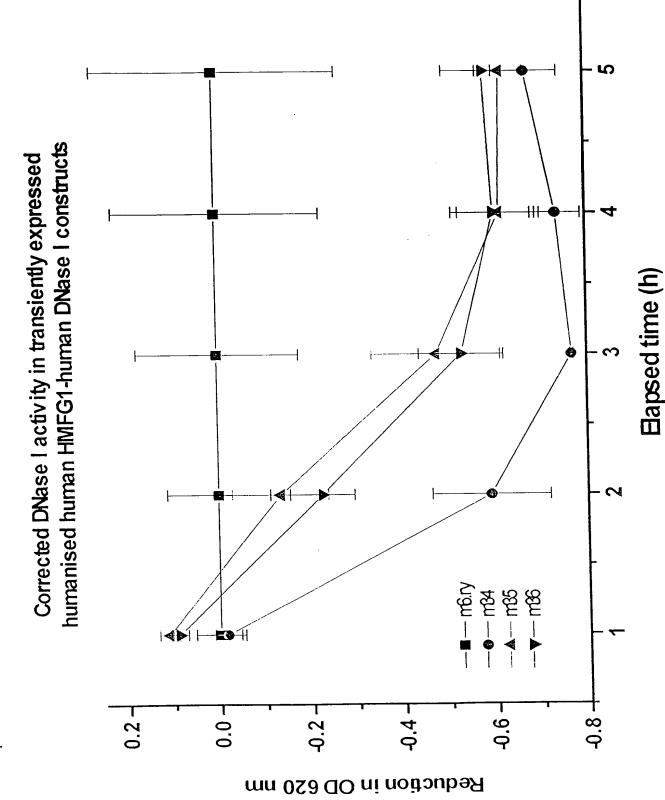


FIG 23

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Corrected DNase I activity in transiently expressed humanised HMFG1 H(ab')2-human DNase I fusions

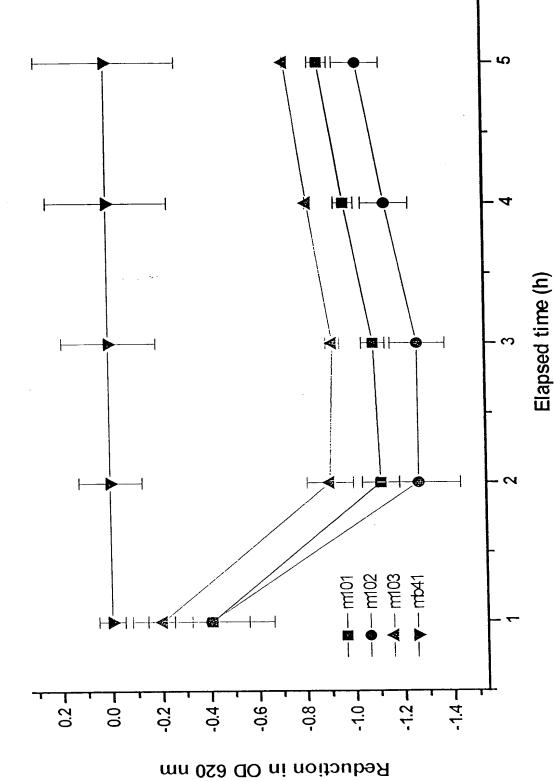
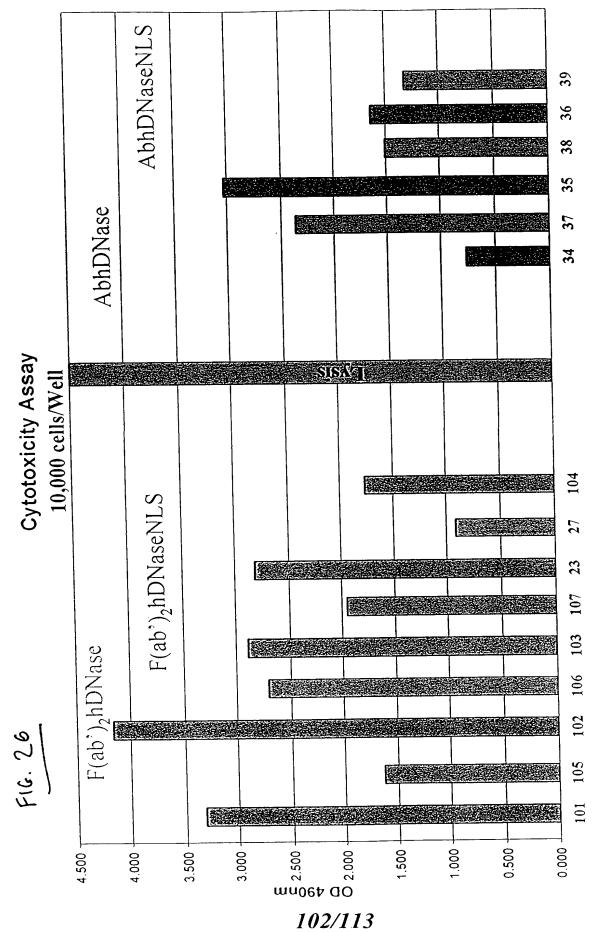


FIG 25

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; }



 $0.097~\mu g/ml$ of each construct

t01

Construct number

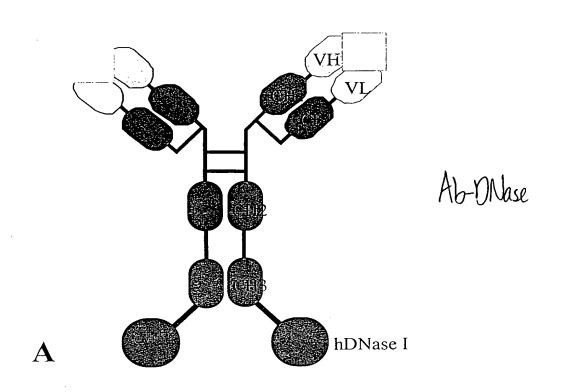
MCF7 cells killed after 1h incubation with 1.35 ng of sample

FIG 27

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% Cells killed

Figure 28



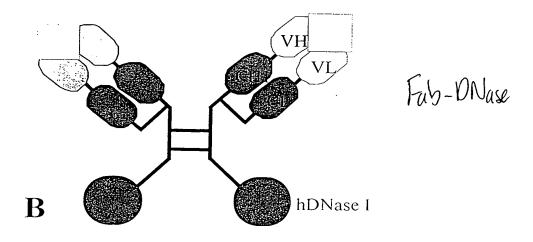
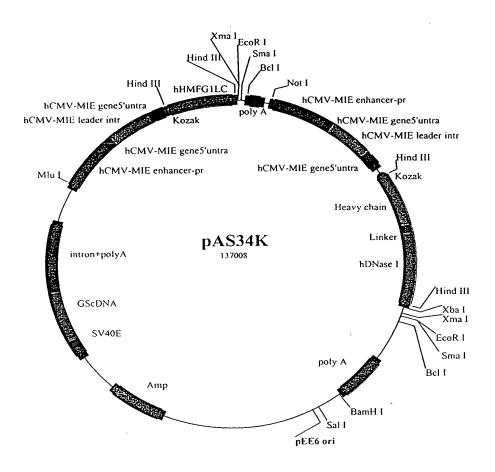
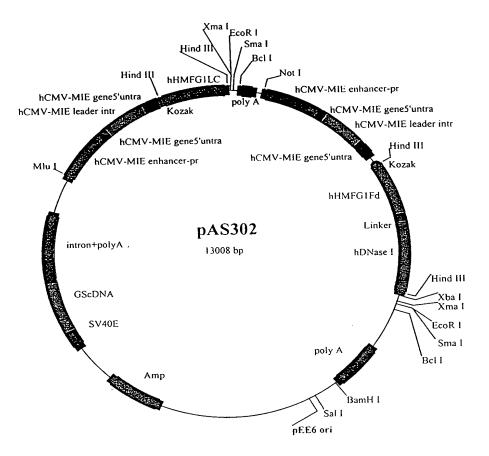


Figure 29



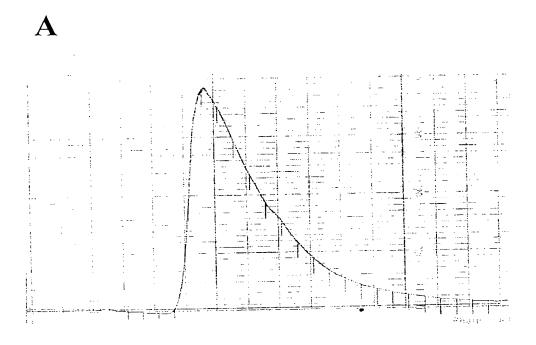
Ab-DNase

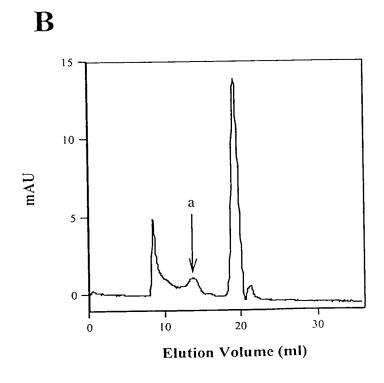
Figure 30



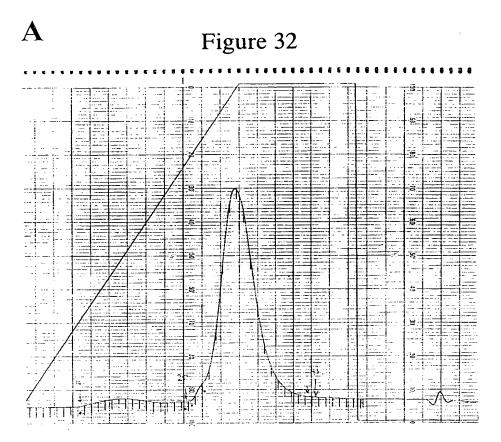
Fab-DNase

Figure 31

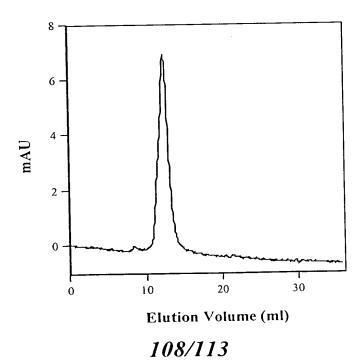


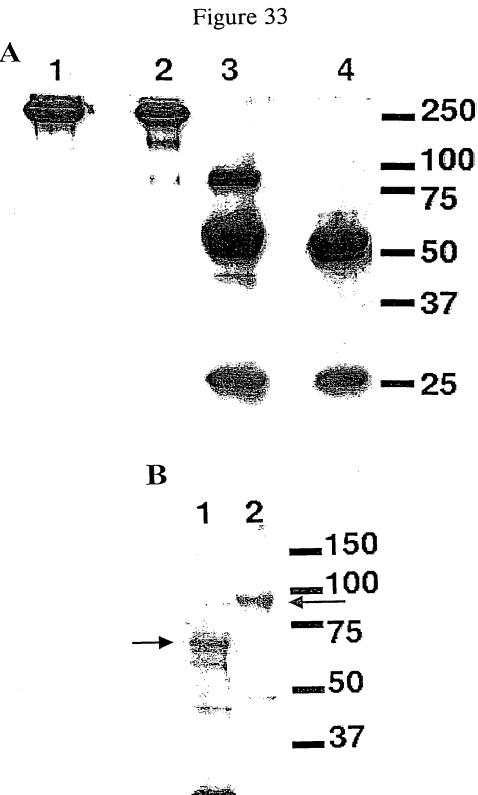


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B

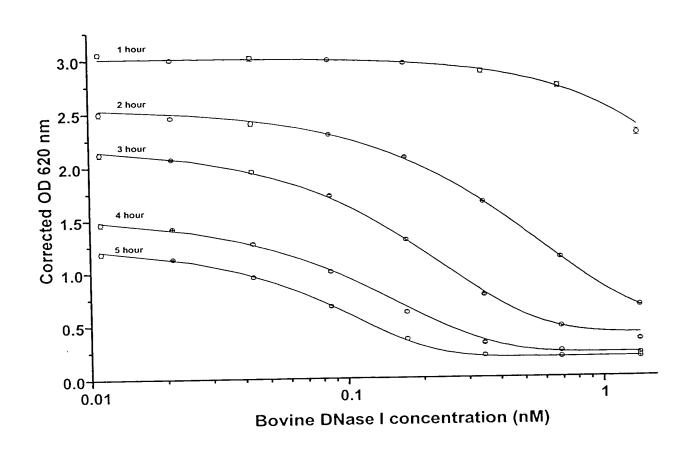




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Figure 34

Bovine DNase I standard curves at various time points



A

Figure 34 – cont.

B

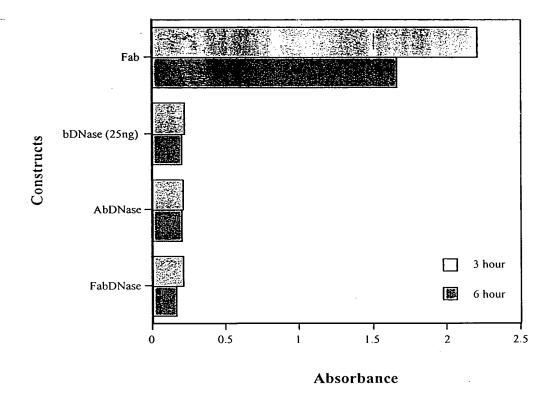
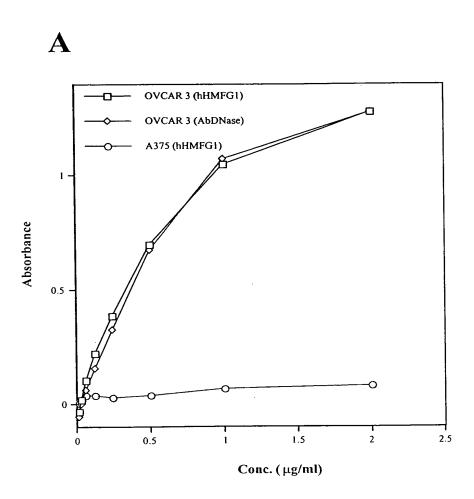
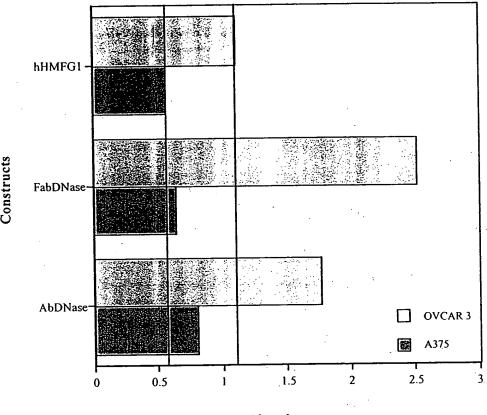


Figure 35



B



Absorbance

YGOO BILABLE COPY